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Perfect score:
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1: /cgnl_7/ptodata/1,
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/cgnl_7/ptodata/1/laa/ECOMB.pep:*
/cgnl_7/ptodata/1/laa/FCTUS_COMB.pep:*
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US-08-488-379-46

PCT-US93-07545-46

US-08-787-547-1

US-08-787-547-33

US-08-787-547-34

US-08-787-547-34

US-08-640-344-6

US-08-640-344-9

US-08-640-344-9

US-08-640-344-9

US-08-468-5408-1

US-08-468-5408-5

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Compugen Ltd
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Query Match 100.0%; Score 171; DB 2; Length Best Local Similarity 100.0%; Pred. No. 4e-160; Matches 171; Conservative 0; Mismatches 0; Indels	US-08-781-122-2 Sequence 2, Application US/08781122 Patent No. 5948764 GENERAL INFORMATION: APPLICANT: Gaur, Amitabh APPLICANT: Conion, Paul J. APPLICANT: Ling, Nicholas TITLE OF INVENTION: UTILIZING PEPTIDE ANALOGUES OF HU UNMER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104-7092 COMPUTER: LBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOUTHARE: PAPLICATION NUMBER: US-OS/MS-DOS SOUTHARE: PAPLICATION UNDER: 31,392 FILING DATE: 09-JAN-1997 CLASSIFICATION INFORMATION: APPLICATION INFORMATION: APPLEATION NUMBER: 31,392 REGISTRATION NUMBER: 31,392 REGISTRATION INFORMATION: TELEPHONE: (206) 682-6031 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 171 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: protein	29 20 11.7 20 3 US-08-470-397-4 30 20 11.7 20 3 US-08-297-395-14 31 20 11.7 20 3 US-08-297-395-15 32 20 11.7 20 3 US-08-297-395-16 33 20 11.7 20 3 US-08-297-395-16 34 20 11.7 20 3 US-08-297-395-19 35 20 11.7 20 3 US-08-297-395-19 36 20 11.7 20 3 US-08-297-395-20 37 20 11.7 20 3 US-08-297-395-21 38 20 11.7 20 3 US-08-297-395-21 38 20 11.7 20 3 US-08-297-395-21 39 20 11.7 20 3 US-08-297-395-22 40 20 11.7 20 3 US-08-297-395-22 41 19 11.1 19 2 US-08-460-344-2 42 19 11.1 19 2 US-08-468-540B-12 44 19 11.1 19 3 US-08-297-395-24 45 19 11.1 19 3 US-08-297-395-24 45 19 11.1 19 3 US-08-297-395-24
th 171; els 0; Gaps 0;	LE SCLEROSIS HUMAN MYELIN BASIC PROTEIN	Sequence 4, Appli Sequence 14, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 25, Appl Sequence 25, Appl Sequence 27, Appl Sequence 29, Appli Sequence 29, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 23, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 21, Appli Sequence 24, Appli

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Best Local S
Matches 170
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APPLICATION NUMBER: US 07/798,099

FILING DATE: 27.WOV-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CA 2,053,799-0

FILING DATE: 22-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Ihnen, Jeffrey L.

REGISTRATION NUMBER: 28,957

REFERENCE/DOCKET NUMBER: 27052-11546;

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                    TOPOLOGY: line MOLECULE TYPE: p
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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62 HHPARTAHYGSLPOKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAEG
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                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                   ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFGGDRGAPKRGSGKDS 61
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                                                                                                                                          99.4%; Score 170; DB 2; L
100.0%; Pred. No. 3.8e-159;
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5194425-4
;Patent No. 5194425
; Patent No. 5194425
; APPLICANT: SHARMA ,SOMESH D.;LERCH, L.
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APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
SEQ ID NO:4:
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Patent No. 5763585
GENERAL INFORMATION:
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Best Local Similarity
Matches 63; Conserv
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CURRENT APPLICATION DATA:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                   APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend
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TITLE OF INVENTION: PURIF
TITLE OF INVENTION: MHC-P
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                                                                                                    APPLICATION NUMBER: US 08/136,216 FILING DATE: 13-OCT-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/367,751 FILING DATE: 21-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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                                               14058-32-1
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                                                                                                                                  TELEFAX: (415) 543-504
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 14058-32-1-1 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 00 FILING DATE: 14-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/470,397
FILING DATE: 06-UUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-CCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Townsend
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MOLECULE TYPE: protein
                            MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Nag, Bishwajit
ITLE OF INVENTION: Purification and Characterization of
INVENTION: MHC-Peptide Complexes Useful in Ameliorating Autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 QDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAEGQ 121
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LOCATION: 1..170
OTHER INFORMATION: /note= "Myelin basic protein"
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                                                                                                                                                                                                                               NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
                                                                TOPOLOGY:
                                                                                STRANDEDNESS
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NAME/KEY:
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Modified-site
                              : protein
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Plaza, Steuart Street Tower,
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0; Mismatches
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; LOCATION: 1.170; OTHER INFORMATION: US-08-470-397-1
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OTHER INFORMATION: 
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 46
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NAME/KEY:
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NAME/KEY:
                                                                       NAME/KEY: Modified LOCATION: 144 OTHER INFORMATION: OTHER INFORMATION:
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LOCATION:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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/note= "Xaa = Gln or absent"
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/note= "Xaa = Ser
                       /note= "Myelin basic protein"
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/note= "Xaa = Ala
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/note= "Xaa = Gly
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/note= "Xaa = Leu
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/note= "Xaa = Ser
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/note= "Xaa = Ser
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/note= "Xaa = Arg
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/note= "Xaa = Leu
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/note= "Xaa = Pro
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/note= "Xaa = Thr
                                                                         /product= "OTHER"
/note= "Xaa = His
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/note= "Xaa = N-a
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GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
TITLE OF INVENTION: PEPTIDES OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION UNMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION UNMBER: 07/502,559
EARLIER FILING DATE: 1993-05-06
EARLIER FILING DATE: 1990-03-30
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER APPLICATION UNMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION UNMBER: 07/065,734
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5194425-3
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AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/367,751
FILING DATE: 21-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
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; APPLICANT: SHARMA ,SOMESH D.;LERCH, L. BERNARD;CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 3
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                                                                                                                Matches
                                                                                                                                          Query Match
Best Local
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Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 41; Conserv
72 SLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLS 111
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                                                                                                                                       Local
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                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                          23.4%; Score 40; DB 3; L
llarity 100.0%; Pred. No. 1.9e-32;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.1e-33;
tive 0; Mismatches 0;
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                                                                                                                                                                  Length 40;
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                                                                                                          Gaps
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US-08-480-190-46
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; APPLICANT: SHARMA, SOMESI
; TITLE OF INVENTION: MHC C
; IN AMELORIATING AUTOIMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 26
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/86
FILING DATE: 14-APR-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 690,840
FILING DATE: 23-APR-1991
                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: Aggust 11, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: ISM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lawrence J. Stern
APPLICANT: JACK L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 576,084
FILING DATE:30-AUG-1990
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
APPLICATION NUMBER: 635,840
FILING DATE: 28-DEC-1998
APPLICATION NUMBER: 367,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-JUN-1989
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1 Similarity 100.0%; Pred. No. 3.4e-18;
26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Clark, Paul 1.
REGISTRATION NUMBER: 30,162
REFERENCE, DOCKET NUMBER: 0024/
TELECOMMUNICATION INFORMATION:
""".FPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                  TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Stroninger
APPLICANT: Jack L. Stroninger
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LENGTH: 24
                                                                                                                                    REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 225 F
CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 GRTQDENPVVHFFKNIVTPRTPPP 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                 STRANDEDNESS
                                                  LENGTH:
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                                                                                                                    (617) 542-8906
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linear
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100.0%; Pred. No.
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                                                                                    46:
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Query Match
Best Local Similarity
Watches 24; Conservat
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PCT-US93-07545-46
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PCT-US93-07545-46
                                                                                                                                                                                                                                                    CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: AUGUST 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 00246/1
REGISTRATION NUMBER: 00246/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                             Matches
                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
                                                                                                                                                                                                                                TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso:
STREET: 225 Franklin Street
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES NUMBER OF SEQUENCES: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 225 F
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 GRTQDENPVVHFFKNIVTPRTPPP 102
                 79 GRTQDENPVVHFFKNIVTPRTPPP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
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                                                                                                                                                                     TYPE: amino STRANDEDNESS:
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1 GRTQDENPVVHFFKNIVTPRTPPP 24
                                                             24;
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Jack L. Strominger
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Dario A. A. Vignali
                                                           Conservative
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                                                                                                                                                      linear
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3ER: 00246/168001
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                                                                          Score 24; pred. No.
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 Mismatches

                                                           Mismatches
                                                                          DB 4;
5.4e-17
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5.4e-17;
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                                                           Indels
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                                                          Gaps
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US-08-787-547-1
; Sequence 1, Application US/08787547
; Patent No. 5783567

RESULT

SENERAL INFORMATION:

APPLICANT:

Hedley, Mary Lynne Curley, Joanne M.

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Patent No. 5785567

GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-787-547-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 13.5%; Score 23; Best Local Similarity 100.0%; Pred. No. Matches 23; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                  Sequence 33,
               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EXITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES F
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
                                                   COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 081
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5783567
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                                                                                                                          225 Franklin Street
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IBM Compatible
                                                                                                                                                                                                    JOANNE M.
ROBERT S.
MICROPARTICLES FOR DELIVERY
OF NUCLEIC ACID
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ROBERT S.
MICROPARTICLES FOR DELIVERY
OF NUCLEIC ACID
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US-08-227-372-4
                                                                                                                                ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/136,216
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
PECTETBATTON NUMBER: 34,774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08227372
Patent No. 5763585
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.3%; Score 21; Best Local Similarity 100.0%; Pred. No. Matches 21; Conservative 0; Mismatci
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 21 amino acids
TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
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NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                          REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-542-5070
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-542-50 TELEPHONE: 617-542-8906
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FILING DATE: 22-JAN-1997
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)GY: linear
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CIT:.
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: BILING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-227-372-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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US-08-787-547-34
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APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEB: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Applications Patent No. 5783567
GENERAL INFORMATION:
                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
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Search completed: September 26, 2000, 19:36:55 Job time: 597 sec

Run

protein on:

Title: Perfect score:

Scoring table: Sequence:

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Post-processing: Listing first 45
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(without alignments)
341.511 Million cell update
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    Myelin basic prote
Human MBP residues
Residues 111-135 o
MBP-2.5 (80-104).
MBP-4 (141-165). M
MBP-5 (101-125). M
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Residues 139-170 o
Residues 142-168 o
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Human basic myelin
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Human myelin basic
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(STRD ) UNIV STANFORD MEDICAL CENT.

(Ref) 6-26834/27.

(Ref) 6-26834/27.

(Ref) 6-26834/27.

(Ref) 6-26834/27.

(Ref) 6-26834/27.

(Ref) 7-26834/27.

(Ref) 7-26834/27.

(Ref) 8-26834/27.

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Best Local Similarity
Matches 171; Conser
                                                             R99580;
07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-NOV-1996 (first entry)
Human myelin basic protein (MBP).
Myelin basic protein; MBP; multiple sclerosis; MS;
inhibition; major histocompatability complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human myelin basic protein Myelin basic protein; MBP; prevention; analogue.
                                                                                                             R99580 standard;
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30-MAY-1996.
16-NOV-1995; U14402.
18-NOV-1994; US-342078.
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                                                                                                                                                                                                                                        121 GQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR
                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                               GQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR 171
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                                                                                                             Protein;
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W43952
W443953
R493953
R95338
R74158
R7554
W37554
W54719
R85137
R85339
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Pred. No. 5.7e-161;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein - has Lysine 91 to treat multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
  competition thymocyte; '
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Myelin basic prote
MBP-2.1 (82-105).
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Human myelin basic
Peptide from Myeli
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MBP-2.6 (80-102).
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16.NOV-1995; U14403.
18.NOV-1994; US-342408.
18.NOV-1994; US-342408.
10.NOV-1994; US-342408.
10.NOV-1994; US-342408.
10.NOV-1994; US-342408.
11.NOV-1994; US-342408.
11.NOV-1994; US-342408.
12.NOV-1994; US-342408.
13.NOV-1994; US-3424
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Best Local :
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W09404121-A.

03-MAR-1994.

17-AUG-1993; U07786.

17-AUG-1992; US-931217.

(AUTO-) AUTOIMMUNE INC.

Hafler DA, Weiner HL;
                                                                      Treating retroviral associated neurological disease - by admin. of by-stander antigen, causing release of transforming growth factor beta from suppressor Tcells
Disclosure; Page 49; 64pp; English.
Myelin basic proteins (sequences R48592-96) and cattle proteolipid protein (R48592) elicit the release of TGF-beta from suppressor Tcells and target the T-cells to neural tissue under cytotoxic attack, thereby reducing neurological disease, e.g. HTLV-1 associated myelopathy, tropical spastic paraparesis and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteolipid protein; myelin basic protein; retrovirus; neurological disease; by-stander antigen; TgG-beta; transforming growth factor-beta; T-cell; T-lymphocyte; myelopathy; paraparesis; human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hafler DA, Weiner WPI; 94-082786/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1994 (first entry)
Human myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R48592 standard; protein;
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                                            infection.
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Pred. No.
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No. 5.7e-161;
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Score 170; DE Pred. No. 5.5 0; Mismatches

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            PD 02-MAY-1995; U13682.
PP 25-OCT-1995; U3-38224.
PR 25-OCT-1995; U3-28224.
PR 25-OCT-1995; U3-404228.
PR 25-OCT-1995; U3-404228.
PR 15-MAR-1995; U3-404228.
PR 15-MAR-1995; U3-404228.
PR 15-MAR-1995; U3-404228.
PR (IMMU-) IMMULOGIC PHARM CORP.
PR (IMMU-) IMMULOGIC PROPERTY PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myelin oligodendrocyte protein.

Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; CD4+; T-cell; autoimmune disease; demyelination; central nervous system; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
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                                                                                                                                                       Query Match
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Matches 113
                                                                                                                                                                                                                 Claim 1; Page 79-80; 156pp; English.

The native human 21.5 kDa foetal isoform (W00399) of myelin basic protein, MBP+X2Cy881, includes an exon 2-encoded region (X2) that may contain an epitope involved in the pathogenesis of multiple sclerosis (MS); the X2 region is not found in the MBP of healthy adults. Recombinant MBP+X2, or variants modified to improve bacterial expression (see also W66107), can be produced in a large scale in bacterial hosts. They are useful for assaying T-cells for responsiveness to MBP epitopes and can be used as therapeutic agents that act by inducing T-cell responses, including anergy and apoptosis, as a means of treating MS.

Sequence 197 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nye SH,
WPI; 96-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human myelin basic protein (foetal isoform).

Myelin basic protein; MBP; MBP+X2Cys81; proteolipid multiple sclerosis; autoimmune disease; diagnosis; t
T-lymphocyte; T-cell; anergy; apoptosis.
W06107 standard;
                                                                                                                                                                                                                                                                                                                                                                   used in the assessment, sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALEX-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1996; U05611.
02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
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                                                           145
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                                                                                                           85
                                                                                                                                 59
                                                                                                                                                       Local Similarity
es 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                         human myelin basic
                       σ
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                                                                                                       KDSHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWG 118
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MJ, Matis L, McFarland HF, Muel Pelfrey CM, Squinto SP, Wilkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALEXION PHARM INC.
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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amino acid, esp. an uncharged amino acid
of mol.wt. below below about 150, partic.
Ser, in constructs of the invention"
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Protein;
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203
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Pred. No. 7.9e-104;
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kins JA;
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t of multiple
                                                                                                                                                                              Length 197;
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therapy;
                                                           197
                                                                                171
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Best Local Similarity 100.0%; Pred. No. 8:
Matches 113; Conservative 0; Mismatches
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07-NOV-1996,
22-APR-1996, U05611.
02-MAY-1995, US-431648.
02-MAY-1995, US-431644.
07-JUN-1995, US-482114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 81-82; 156pp; English.

A 21.5 kDa foetal isoform (W06107) of myelin basic protein, MBP+X2Cy881/Dact., is the product of a DNA construct (T4.1896) based on the human foetal MBP+X2Cy881 isoform (W00399) but utilising bacterially-preferred codons in place of the native human codons (see also T41889). This increases prodn. of the MBP in E. coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also W00399 and W06108) are useful in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                           Foetal myelin basic protein MBP+X2Ser81/
Myelin basic protein; MBP; MBP+X2Ser81;
multiple sclerosis; autolamune disease;
T-lymphocyte; T-cell; anergy; apoptosis.
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Foetal myelin basic protein MBP+X2Cys81/bact.
Myelin basic protein; MBP; MBP+X2Cys81; prote
multiple sclerosis; autoimmune disease; diagr
T-lymphocyte; T-cell; anergy; apoptosis.
  WO9634622-A1.
07-NOV-1996.
                                                                                                                                                                  T-lymphocyte;
Synthetic.
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(USSH) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McFarland HF, Muel
Lenardo MJ, Matis L, McFarland HF, Muel
Nye SH, Pelfrey CM, Squinto SP, Wilkins
WPI, 96-505898/50.
                                                                                                                                                                                                                                                               W06108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human myelin basic protein and used in the assessment, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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01-FEB-1997
                                                                                                                                       region
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                                                                                                                                                                                                                                                               standard;
                                                                                           /label= X2
/note= "exon
mutation"
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/note= "
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                                     /label= Hexa-histidine_tag
/note= "the hexa-histidine tag i
purification of the recombinant
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                               Protein;
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lkins JA;
                                                                                                          region,
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diagnosis; therapy;
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diagnosis; t
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t of multiple
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therapy;
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Best Local S
Matches 113
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02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
(ALEX-) ALEXION PHARM INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McFarland HF, Mueller EE
Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
WPI; 96-505898/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A 21.5 kDa foetal isoform (W06108) of myelin basic protein, MBP+XSer81/Dact, is the product of a DNA construct (T41897) based on the human foetal MBP+XCys81 isoform (W00399) but utilising codons that are highly expressed in bacterial genes i place of the native codons (see also T41889) and incorporating sequence coding for a hexa-histidine tail. This allows large-scale prodn. and purification of the MBP in bacterial hosts. Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) useful in the clinical assessment, diagnosis and treatment of Marchael and Marchael assessment, diagnosis and treatment of Marchael assessment, diagnosis and treatment of Marchael assessment.
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                                                                                                                                                                                                                                                                                       peptide
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Proteolipid
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A 21.5 kDa foetal isofo
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                                                                                                                                                                                                                                                                                                                            domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   himera (MBP21.5-delta PLP4 fusion).
olipid protein; PLP; delta PLP3; myelin basic protein; MBP;
.5; multiple sclerosis; autoimmune disease; diagnosis;
py; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA;
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                                                                                                                                                                     /label- Epitope
/note- "PLP epitope
210. .230
                                                                                                                                                                                                                                                               /note-
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201. .3
                   /label= Epitope
/note= "PLP epi
                                                                        /label= Epitope
/note= "PLP epitope
                                                                                                                                                      /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                  note "PLP
                                                                                                                                                                                                                                                                                                                                                                                /label- MBP21.5
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                                                                                                                                                                                                                                            te= "synthetic N-terminal
native protein"
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PLP epitope
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                   epitope
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Pred. No.
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8.1e-104;
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c of multiple
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                   sclerosis
Claim 34; Page 110-112; 156pp; English.
MP4 chimera (W06103) is a fusion protein composed of human myelin
basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lack;
all 4 hydrophobic domains of native human PLP (W06106) but
all 4 hydrophobic associated with multiple sclerosis (MS). I
                                                                                                                                                                                                                                                                                                  22-APR-1995;
02-MAY-1995;
02-MAY-1995;
07-JUN-1995;
                                                                                                                                                                                                        (ALEX-)
(USSH )
Lenardo
Nye SH,
WPI; 96-
                                                                                                                                              New human myelin basic used in the assessment,
                                                                                                                                                                                                                                                                                                                                                                              WO9634622-A1.
07-NOV-1996.
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                                                                                                                                                                                                        96-505898/50.
                                                                                                                                                                                                                      ALEXION PHARM INC.
US DEPT HEALTH & HUMAN SERVICES.
MJ, Matis L, McFarland HF, Mu
Pelfrey_CM, Squinto SP, Wilkin
                                                                                                                                                                                                                                                                                                    US-431648.
US-431644.
US-482114.
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/note= "PLP epitor"
270. .303
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/note- "PLP
248. 269
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/note= "hexa-histidine
protein purification"
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369. .:
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/note= "PLP epi
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/note- "PLP epitope
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/note= "PLP epi
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/note= "PLP epitope
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/note= "PLP epitope
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/note- "PLP epi
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/note= "PLP epitope
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373
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Wilkins JA;
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373

Query Match Best Local Sin Matches 113;

Similarity

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W06104; W06104

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can be expressed in E. coli transformants using a DNA construct (T41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera and other novel PLPP/MBP21.5 polypeptides (W00399-400, W06101-08) are useful for the clinical assessment, diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PM4 chimera (delta PLP4-MBP21.5 fusion).
Proteolipid protein; PLP; delta PLP4; myelin basic protein;
MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
therapy; T-lymphocyte; T-cell; PM4 chimera.
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ilarity 100.0%;
Conservative
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 /label= Epitope
/note= "PLP epitope associated with
93. .108
                                                                                                                                   58. .71
/label= Epitope
/note= "PLP epitope
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/note= "PLP epitope
45. .58
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/note = "PLP epitope
42..62
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/note= "PLP epitope
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/note- "PLP epitope
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1.3e-103;
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Matches 113; Conserv
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07-NOV-1996,
22-APR-1996; U05611.
02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
                                                                                                                                                           PM4 chimera (W05104) is a fusion protein composed of delta PLP4 (W05101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein (PLP) mutein that lacks all 4 hydrophobic domains of native human PLP (W05106) but includes PLP epitopes associated with multiple sclerosis (WS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP) associated with MS. PM4 is in reverse orientation to MP4 chimera (W05103). It can be expressed in bacterial host cells using a DNA construct (T41894). PLP polypeptides (see also W00400, W05101-03 and W05105) can be used in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                                                                                                                                                                                                                (ALEX-) ALEXION PHARM INC.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matts L, McFarland HF, Mueller
Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
WPI: 96-505898/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
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AEGQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR
                                                      KDSHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWG
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                                                                                            Conservative
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152. .166
/label= Epitope
'^~te= "PLP epitope ₹
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/note- "encephalitogenic
57, .70
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/note= "PLP epi
96. .107
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/label= Histidine_tag
/note= "hexa-histidine tag
protein purification"
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/note= "PLP epitope
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/note= "PLP epitope
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/note= "PLP epitope
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note "PLP epitope
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"encephalitogenic
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1.3e-103;
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/note= 49. .7

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Best Local S
Matches 113
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07-NOV-1996;
22-APR-1996; U05611.
02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
                                                                                                                                                                                                                                                                                                                                                         are useful
of MS.
Sequence
              O1-FEB-1997 (first entry)

MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion).

Proteolipid protein; Pick; delta PLP4; myelin basic

MBP21.5; multiple sclerosis; autoimmune disease; di

therapy; T-lymphocyte; T-cell; MMOGP4 chimera;

myelin oligodendrocyte glycoprotein; MOG.
                                                                                   W06105;
01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                 Claim 33; Page 108-110; 156pp; English.

MP3 chimera (M06102) is a fusion protein composed of human myeli
basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
delta PLP3 (W00400), a proteolipid protein (PLP) mutein that lac
hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but
includes PLP epitopes associated with multiple sclerosis (MS).
can be expressed in E. coli transformate using a DNA construct
(T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera
and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)
after useful for the clinical assessment, diagnosis and treatment
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Proteolipid protein; PLP; delta PLP3; myelin basic protein; MB proteolipid protein; PLP; delta PLP3; myelin basic protein; MB proteolipid protein; MB autoimmune disease; diagnosis; MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; multiple sclerosis; multiple
    Synthetic.
                                                                                                        W06105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nye SH, Pelfrey CM, WPI; 96-50580075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   )2-MAY 1995; US-482114.
)7-JUN-1995; US-482114.
(ALEX:) ALEXION PHARM INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McFarland HF, Muel
Lenardo MJ, Matis L, McFarland WF, Muel
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mes 113; Conser
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                                                                                                                                                                               AEGQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSK1FKLGGRDSRSGSPMARR
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23-APR-1992; U03391.
23-APR-1991; US-690840.
(ANER-) ANERGEN INC.
(ANER-) LETCH BL, Shi
WPI; 93-036056/04.
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MMOGP4 chimera (W06105) is a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutein. MBP21.5, PLP and MOG are all recognised by autoreactive T cells from multiple sclerosis (MS) patients. The chimera was produced using a DNA construct (M1895) obtd. by inserting a sequence encoding the MOG moiety into MP4 chimera DNA (see also T41893). MMOGP4 chimera can be expressed in bacterial cell hosts. PLP and MBP polypeptides (see also W00400, W06101-04, W06107-08) are useful in the clinical assessment, diagnosis and treatment of MS.
           immune response such as auto:immunity Claim 30; Page 68 + Fig 7; 93pp; English.

A method is claimed for the prepn. of a pure major MHC-peptide complex. The MHC component is a Class II glycoprotein of the and the peptide comprises amino acids 1-14 of MBP.

Sequence 170 AA;
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02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
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Lenardo MJ, Matis L, McFarland HF, Mueller
                                                                                                                                                                                                                    Pure major MHC-peptide complex -
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15-OCT-1991; CA-053799.
22-OCT-1991; CA-053799.
(CATZ/) CATZ I.
(WARR/) WARREN K G.
(CATZ I. WARTEN KG;
WPI; 93-152422/18.
                                                                                                                                   Homologous peptide analogues of human basic myelin protein - us for treating multiple sclerosis
Disclosure; Fig 4, 26pp: English.
The sequence is that of human basic myelin protein (BMP). Frag of this sequence are claimed (see features) which are able to neutralise anti-BMP antibodies and are thus useful in treatment multiple sclerosis. The fragments may be prepd. Synthetically avoids the dangers associated with the use of the natural prote e.g. transmission of neuroviruses. Also the peptides are too sequence 170 AA;
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BMP; MS; multiple sclerosis; homologue;
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DAQGTLSKIFKLGGRDSRSGSPMARR
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                                                                      15-OCT-1998: CA0290: 03-APR-1998; CA-201841. 04-APR-1997; CA-201841. (UYAL-) UNIV ALBERTA. Catz I, Warren KG; WPI; 98-568336/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent claims complexes of formulae (I), (II) and (III) which are as follows: (I) x - MCH - peptide; (II) MHC - peptide - x; (III) MHC - peptide. The peptide - x; (III) MHC - peptide. Where x - toxin or labelling gp; MHC - effective portion of the major histocompatibility glycoprotein; and the peptide includes an epitope associated with one of the major autoimmune diseases, including multiple sclerosis (MS). MBP is the principle autoantigen in MS and is a candidate peptide for insertion in the complexes which can be used to treat and monitor MS. Pertinent sections of MBP are determined empirically, using a strain of mice which develops experimental allergic encephalities when immunised with bovine MBP. The sequence given in p94717 is with the substitution of the residues above the sequence in Fig 7. The sequence without substitutions is given in p92226.
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23-JUN-1989; U02784.
21-JUN-1989; US-367751, US-210594.
(BIOS-) Biospan Corp.
Sharma SD, Lerch LB, Clark BR;
                  Peptide and its derivatives for treatment of multiple sclerosis capable of neutralising or modulating production of anti-myelin
                                                                                                                                                                                                                                                             Homo sapiens. W09845327-A1.
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basic
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Human myelin basic protein fragment.
Human; myelin basic protein; MBP; multiple scierosis; anti-MBP; MS
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Best Local Similarity
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The present sequence represents a myelin basic protein (MBP) protein fragment used to produce MBP peptides. MBP peptides are capable of neutralising or modulating the production of anti-myelin basic protein. The present invention also describes a method for treating multiple sclerosis (MS). The method comprises administering to the patient an MBP peptide of the formula: R1-Val-His-Phe-Phe-Lys-Asn-Ile-R2 where R1, R2 = H, OH, or an amino acid residue and a polypeptide residue, provided that R1 and R2 are not both H or OH at the same time.

Sequence 46 AA;
                                     62
                    HHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKG 107
HHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKG
                                                                      26.9%;
ilarity 100.0%;
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/db_xref="danazo11.1"
/db_xref="d1:435062"
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GFLPRHRDTGILDSTGRFFGGDRGAPKRGSGKDSHHPARTAHYGSLPQKSHGRTODEN
PVVHFFKNIVTPRTPPPSOGKKGRGLSLSRFSWGAEGORPGFGYGGRASDYKSAHKGFK
GTVARGTKSKIFKLGGRDSRSGSPWARR"
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I (bases 1 to 1781)
Pribyl, T. M., Campagnoni, C. W., Kampf, K., Kashima, T., Handley, V. W., McMahon, J. and Campagnoni, A. T.
                                                                                                                                                                                                                        08-MAR-1994
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Proc. Natl. Acad. Sci. U.S.A. 90 (22), 10695-10699 (1993)
94068468
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  L00403 N
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M11529 N
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Human Golli-mbp gene, complete cds.
L18866
L18866.1 GI:435061
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341. .553
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                                                                                                                                       seq_name: gb_pr2:HUMRNAMBPF
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Homo sapiens
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gb_ro:MUSMBPMLD2
     gb_ro:MUSMBPA6
                                                                                                                                                                                                                                                                                                VERSION
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1 X17369 H.saplens MBP gene, exon
1 X7290 H.saplens MBP gene, exon
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1 M11532 Mouse myelin basic prote
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Mouse myelin basic prote
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                                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
     out_format : pfs
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9b_pr2: HUMMBPA

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9b_pr2: HUMMBP1/R

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9b_pr2: HUMMBPB

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9b_ro: RATMBP1A

9b_ro: RATMBP1A

9b_ro: HUMRNAMBPE

9b_ro: MUSMBP1A

9b_ro: HUMMBP1A

9b_pr2: HUMMBP1A

9b_pr2: HUMMBP1A

9b_pr2: HUMMBP1A

9b_pr3: APO0110

9b_hr91: APO01649

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9b_ov: SRD44 052
9b_ro: MUSCOLLIC
9b_htg1: AP001853
9b_htg1: AP001649
9b_om: AF010432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                                                                                                                                                      601 ATGCCGTCACAGAAGACCCTCCCAGAGCCACGGATCCAAGTACCTGGC 650
                                                                                                                                                                                                                                                                                                                                701 GAGACACGGCATCCTIGACTCCATCGGGCGCTTCTTIGGCGGTGACAGG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
                                                                                                                                                                                                                                                                         1 MetAlaSerGlnLysArgProSerGlnArgH1sGlySerLysTyrLeuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG
                                                                                                                                                   Length: 171
Gaps: 0
Percent Identity: 100.000
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1117. .>1781
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                                                                                  492 g
                                                                                                                                                                                                                                                 Align seg 1/1 to: HUMRNAMBPF
                                                                                 545 c
                                                                                                                                                                                                         alignment_block:
US-09-218-277-12 x HUMRNAMBPF
                                                                                                                                                                 Ratio: 5.392
Percent Similarity: 100.000
                                                                                                                                                    922.00
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LOCUS HUMMBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr2:HUMMBPA
                                                                                                                                                    Quality:
Ratio:
                                                                                 427
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                                                      3'UTR
                                                                                 BASE COUNT
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FFGGDRGAPKRGSGKDSHHPARTANYGSLPQKSHGRTQDENPVVHFFKNIVTPLDSJGR
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                                 Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2139)
Kamholz,J., de Ferra,F., Puckett,C. and Lazzarini,R.
Identification of three forms of human myelin basic protein by
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                                                                                             cloning
Proc. Natl. Acad: Sci. U.S.A. 83 (13), 4962-4966 (1986)
86259714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519 a 619 c 556 g 445 t
Chromosome 18q22-qter; 1212 bp upstream of EcoRI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 171
Gaps: 0
Percent Identity: 100.000
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    . 2139
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    /db_xref="taxon:9606"
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    /note="MBP mRNA"

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                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /gene="MBP"
37. .552
/gene="MBP"
                                                                                                                                                                                                                                                                                                     37. .552
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Ratio: 5.392
Percent Similarity: 100.000
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

I bases 1 to 1261)

Roth, H.J., Kronquist, K.E., Kerlero de Rosbo, N., Crandall, B.F. and Campagnoni, A.T.

Evidence for the expression of four myelin basic protein variants in the developing human spinal cord through cDNA cloning J. Neurosci. Res. 17 (4), 321-328 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMMABPC 1261 bp mRNA PRI 07-JAN-1995
Human 21.5 kD myelin basic protein (RK41) mRNA, complete cds. M30515.
M30515.1 GI:187412
alternative splicing; myelin basic protein.
Human spinal cord, cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eLysAsnileValThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 .. LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
                                                                                                                 4 ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyPheGlyTyrGlyGlyArgalaSerAspTyrLysSerAlaHisLysGl
                                                                          1 MetalaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
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                                                                                                                                                                                                                                                                                                       51 GlyAlaProLysArgGlySerGly......
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1. .1261
                                       Align seg 1/1 to: HUM215MBP
 US-09-218-277-12 x HUM215MBP
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LOCUS HUMMBPC
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 622)
Nye,S.H., Pelfrey,C.M., Burkwit,J.J., Voskuhl,R.R., Lenardo,M.J.
and Mueller,J.P.
Purification of immunologically active recombinant 21.5 kDa isoform
Of human myelin basic protein
Mol. Immunol. 32 (14-15), 1131-1141 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation-"MASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGR
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YKSAHKGFKGVDAQGTFFKLGGRDSRSGSPMARRHHHHHH"
220 167 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                      HUM215MBP 622 bp DNA PRI 20-JAN-1996
Homo sapiens synthetic myelin basic protein 21.5 kDa isoform gene,
complete cds.
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Location/Qualifiers

L. 622

/organism="Homo sapiens"
//db_xref="taxon:9806"
//map="lsynthetically derived in the laboratory with cligoniclectides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (sites)
Kamholz,J., de Ferra,F., Puckett,C. and Lazzarini,R.
Identification of three forms of human myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="21.5 kDa isoform; bp 595-612: histidine tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
86259714
                                   synthetic DNA; synthetic gene
387 GGGGCCGAAGGCCAGAGCCAGGATTTGGCTACGGAGGCAGAGCGTCCG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 1
Percent Identity: 86.802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="myelin basic protein"
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myelin basic protein;
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5.257
86.802
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Homo sapiens
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                                                                                                                                                                                                                           537 CATGGCTAGACGC 549
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Ratio:
Percent Similarity:
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source

FEATURES

gene

JOURNAL MEDLINE COMMENT

BASE COUNT

ORIGIN

DEFINITION

167

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

MEDLINE REFERENCE AUTHORS

TITLE

JOURNAL

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158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg
                                                                                                             LOCUS
DEFINITION
ACCESSION
                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                              /translation-"MASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGR
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YKSAHKGFKVVDAGTYSKTFKJGRDSRSGSPMARR"
378 c 336 g 259 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eLysasnileValThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 CACAGCAAGTACCATGGACCATGCCAGGCATGGCTTCCTCCCAAGGCACA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 CAAGAACATIGIGACGCCTCGCACCACCCCCCGTCGCAGGGAAAGGGGA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aThralaSerThrMetAspHisalaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ATGGCGTCACAGAAGACCCTCCCAGAGGCACGGATCCAAGTACCTGGC 57
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Percent Identity: 86.802
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/organism="Homo sapiens"
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/map="18q22-qter"
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                                         /gene="MBP"
8
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5.257
86.802
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Ratio:
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                                                                                                                                                                                                                      BASE CO
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SQGKGAEGQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR
                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 1172)

Roth, H.J., Kronquist, K., Pretorius, P.J., Crandall, B.F. and Campagnoni, A.T.

Isolation and characterization of a CDNA coding for a novel human 17.3K myelin basic protein (MBP) variant

J. Neurosci. Res. 16 (1), 227-238 (1986)
                                                                                                                         HUMMBP17K 1172 bp mRNA PRI 07-JAN-1995
Human 17.3K myelin basic protein (MBP) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
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                                                                                                                                                                                  M30047.1 GI:187400
myelin basic protein.
Human fetal spinal cord, cDNA to mRNA, clone KK36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GlyalaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 GGTGCGCCCAAGCGGGGCTCTGGCAAGGACTCACACCCGCGGAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 AIGGCGICACAGAAGACCCICCCAGAGGCACGGAICCAAGIACCIGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 aThralaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA
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Gaps: 1
Percent Identity: 93.567
to: 1172
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33. 515
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5.297
93.567
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US-09-218-277-12 x HUMMBP17K
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                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                     seq_documentation_block:
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                86308101
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Percent Identity: 93.605

97.674

Wed Sep

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Percent Similarity:
                                                                     Align seg 1/1
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VERSION
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AUTHORS
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KGRGLSLSRFSWGAEGQKPGFGYGGRASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDS
                                                                                                                                                                                                                                                                                                                                                                                                               RNO132897 510 bp mRNA ROD 11-FEB-1999 Rattus norvegicus mRNA for myelin basic protein, 18.5 kDa isoform. AJ132897. GI:4454314 isoform: mbp gene; myelin; myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute, Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 510)
                                                                                                          84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
                                                      ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
                                                                                                                                                                                                                                                                LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
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Lobell, A.M. and Wigzell, H.
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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155 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                   167 OMEtAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                     seq_name: gb_ro:RNO132897
                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS RN0132897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lobell, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
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DEFINITION
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TITLE
JOURNAL
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AUTHORS
JOURNAL
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                                                                                              101
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172

Length: Gaps:

836.00 4.976

Quality: Ratio:

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Losses I to 1231)
Roth, H.J., Kronquist, K.E., Kerlero de Rosbo, N., Crandall, B.F. and Campagnoni, A.T.
Evidence for the expression of four myelin basic protein variants in the developing human spinal cord through cDNA cloning J. Neurosci. Res. 17 (4), 321-328 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMMBPB 1231 bp mRNA PRI 07-JAN-1995
Human 20.2 kD myelin basic protein (RK187) mRNA, complete cds.
M30516
M30516.
M30516.1 G1:187410
alternative splicing; myelin basic protein.
Human spinal cord, cDNA to mRNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGCCGAGGGGCAGAAGCCAGGATTGGCTACGGAGGCAGAGCTTCCG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SpTyrLysSerAlaHisLysGlyPheLysGlyVal...AspAlaGlnGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
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                                                                                                                                                                                                                                                                                                                                                                                                                67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
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                                                          from: 1
                                                        to: RN0132897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 ICCCATAGCAAGACGC 507
alignment_block:
US-09-218-277-12 x RN0132897
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LOCUS HUMMBPB
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MEDLINE
· FEATURES
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DEFINITION
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ORIGIN
                                                                                                                                                                         REFERENCE
AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                     211 GAGCCCTCTGCCCTCTATGCCCGCAGCCTGGGGCTGTGCAACATGT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 GGTGCGCCCAAGCGGGGCTCTGGCAAGGTACCCTGGCTAAAGCCGGGCCG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 GlnLysSerH1sGlyargThrGlnAspGluAsnProvalValH1sPhePh 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 2
Percent Identity: 81.218
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US-09-218-277-12 x HUMMBPB
                                                                                                                                                                                                                    Quality:
Ratio:
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                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                               BASE COUNT
                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28
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                                        SGS
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Norway rat.

SM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

E (bases 1 to 588)

Meissert,R., Lobell,A.M., de Graaf,K.L., Eltayeb,S.Y.,

Andersson,R., Olssen,T. and Wigsell,H.

Protective DNA vaccination against organ-specific autoimmunity is highly specific and discriminates between single amino acid substitutions in the peptide autoantigen

L Proc. Natl. Acad. Sci. U.S.A. 97, 168-1694 (2000)

E 2 (bases 1 to 588)

L Debl.A.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute, Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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AJ132898.1 GI:4454316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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US-09-218-277-12 x RNO132898
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4.839
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                                                                                                                                                                                   seq_name: gb_ro:RNO132898
                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS
RN0132898
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/db_xref="GI:3309629"
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134 c 122 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS MCMBP78M 1939 bp mRNA ROD 15-AUG-1995
DEFINITION MOUSE myelin basic protein mRNA, 3' end, clone NK-M78.
ACCESSION M15062
VERSION M15062.1 GI:199050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 1939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heLysAsnIleValThrProArgThrProProProSerGlnGlyLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oGlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPheP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyLysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPr
                                                                                                                                                                                 Percent Identity: 91.558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alternative splicing; myelin basic protein. Mus musculus (strain C57BL/6J, sub_species NK-M78.) 18-day-old brain cDNA to mRNA. Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1909)
Newman,S., Kitamura,K. and Campagnoni,A.T.
                                                                                                                                                    Length:
                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                               to: 450
                                                                                                                                                                                                                                                             Align seg 1/1 to: AF074337 from: 1
                                                                                                                                                  724.50
4.895
96.104
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Ratio:
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                                                                                                                                   alignment_scores
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ACCESSION
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                                                                     BASE COUNT
ORIGIN
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AUTHORS
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Cavia porcellus'
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.

1 (bases 1 to 450)
Kim.G., Tanuna.N. and Matsumoto,Y.
DNA vaccination using Guinea pig myelin basic protein coding region in experimental autoimmune encephalomyelitis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 450)
Kim.G., Tanuma.N. and Matsumoto,Y.
Direct Submission
Submitted (24-JUN-1998) Neuropathology, Tokyo Metropolitan
Institute for Neuroscience, Musashidai 2-6, Fuchu, Tokyo 183-8526,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF074337 450 bp mRNA ROD 14-JUL-1998
LOCUS AF074337 A50 bp mRNA partial cds.
ACCESSION AF074337.1 GI:3309628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
                                       eLysasnileValThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                       141
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                                                                                                                                                                              294
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                                                                                                                                                                   GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGl
                                                                                                                                                .. LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro
                                                                                                                                                                                                             GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh
                                                                                                                                                                                                                                                                                                                                                                                                                                     442 GGATTTGGCTACGGAGGCAGACTTCCGACTATAAATCGGCTCACAAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="myelin basic protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .450
/organism="Cavia_porcellus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Hartley"
/db_xref="taxon:10141"
/tissue_type="spinal cord"
<1. .>450
                     GlyAlaProLysArgGlySerGly......
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/gene="MBP"
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74

57

24 20 247 107

1

124 347 domesticus) (clone:

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51 GlyalaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS RATMBP2A
                                                                                                                                                                                                                                                                                               seq_name: gb_ro:RATMBP2A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="rskylatastmdharhgflprhrdjildsigrefsgdrgapkr
GSGKDSHTRTTHYGSLPQKSQHGRTQDENPVVHFFKNIVTPRTPPPSQGKGAEGQKPG
FGYGGRASDYKSAHKGFKGAYDAQGTLSKIFKLGGRDSRSGSPMARR"
                                                                   Draft entry and computer-readable sequence for [1] kindly provided by A.T.Campagnoni, 30-MAR-1987.

By A.T.Campagnoni, 30-MAR-1987.

By A.T.Campagnoni, 30-MAR-1987.

By and yas eight myelin basic proteins can be encoded by the same gene by alternative splicing. The sequence below is missing exons 2 and 5 of the gene and encodes a 17.22 kba myelin basic protein. The variations in the 3' untranslated regions between the two clones may be reverse transcriptase errors [1].

Location/Qualifiers
Identification of a cDNA coding for a fifth form of myelin basic
                  protein in mouse
Proc. Natl. Acad. Sci. U.S.A. 84 (3), 886-890 (1987)
87118269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGCGGTGACAGGGGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 alThrProArgThrProProProSerGlnGlyLysGlyArgGlyLeuSer 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 LeuSerArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTy 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 sGlyArgThrGlnAspGluAsnProValValHisPheDysAsnIleV 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 TGACACCTCGAACACCACCTCCATCCCAAGGGAAG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 87.578
                                                                                                                                                                                                                                                                                                                                                                                                               /note="myelin basic protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="t in M78; c in M72"
                                                                                                                                                                                                                                                                                         /sub_species="domesticus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB59712.1"
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                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="brain"
<1. .452
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=3
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1700
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4.908
90.683
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US-09-218-277-12 x MUSMBP78M
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Ratio:
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                                                                                                                                                                                                                    FEATURES
TITLE
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FFSGDRGAPKRGSGRDSHTRTHYGSLPQKSQRTQDENPVVHFFKNIVTPRTPPPSQG
KGRGLSISRFSWGGRDSRGSPARRR"
195 c 148 g 118 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                    27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaria; Metazoa; Chordata; Craniata; Vertebrata; Mammal Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus I (bases I to 612) Schalch, M., Budzinski, R.-M. and Stoffel, W. Cloned proteolipid protein and myalin basic pritein cDNA: Transcription of the two genes during myelination Biol. Chem. Hoppe-Seyler 367, 825-834 (1986)
                                                      145 al... AspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyGlyArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAGG 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                             myelin basic protein.
Rat (18-day old) brain, cDNA to mRNA, clone pMBP2.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg
Rat myelin basic protein mRNA, complete cds. M25889
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Gaps: 3
Percent Identity: 72.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41. .427
/note="myelin basic protein"
/codon_start=1
                                                                                                                                                                                                                                                417 GACAGCCGCTCTGGATCTCCCATGGCGAGACGC 449
                                                                                                                                                                                                                           161 AspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .612
/organism="Rattus no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
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alignment_scores:

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84026484 mbp's have been found in rats, small (m-r=14,000) and large (m-r=18,500), the sequence shown is for the small mbp, however the.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200; Chordata; Craniata; Vertebrata; Mammalia;
tia; Sciurognathi; Muridae; Murinae; Rattus.
1464)
1.K.B., Horvath,S., Prusiner,S.B. and Hood,L.E.
1 of cloned odna representing rat myelin basic
3 of expression in brain of shiverer mutant mice; (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1993
                                                                                                                                                                                                                                                                                                                                             ProGInLysSerHisGlyArgThrGlnAspG 84
                                                                                                                                                                                                                                                                                                                                                                                                     342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euGlyGlyArgAspSerArgSerGlySerPr 167
                                                                                                                                                                                            erGlyLysAspSerH1sHisProalaArgTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sGlyPheLysGlyValAspAlaGlnGlyThr 150
                                                                                                                        HisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ley, newborn) cdna to brain mrna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 171
Gaps: 3
Percent Identity: 71.930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 bp mRNA ROD : protein (mbp) gene mrna.
                                                                                              5 from: 1 to: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
COMMENT
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Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 2256)
S Gundelfingar, E.D.
Direct Submission
L Submitted (08-NOV-1989) Gundelfinger E. D., Universitaet Hamburg, Universitaetskrankenhaus Eppendorf, Zentrum fuer Molekulare Neurobiologie, Martinistrasse 52, 2000 Hamburg 20, FRG
E (bases 1 to 2256)
S Zopf, D., Sonntag, V., Betz, H. and Gundelfinger, E.D.
Developmental accumulation and heterogeneity of myelin basic protein transcripts in the chick visual system
E 99358239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MASQKRSSFRHGSKMASASTTDHARHGSPRHRDSGLLDSLGRFF
GGDRHVPRRGFGKDIHAARASHVGSIPQRSQHGRPGDDNPVVHFFKNIVSPRTPPPMQ
AKGRGLSLTRFSWGGEGHKPGYGSGKFYEHKSAHKGHKGSYHEGQGTLSKIFKLGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetalaSerGlnLysArgProSerGlnArgH1sGlySerLysTyrLeuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                            6. .530
/note="myelin basic protein (AA 1-174)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .2256
/organism="Miles gallus"
/organism="Walles leghorn"
/db_xref="taxon:9031"
/dev_stage="day 1 post hatching"
/ilssue_type="brain optic lobe"
/clone_lip="longodendrocytes"
/clone_lib="lambda gil0"
/clone="0219/10, 0219/2/3, 0219/2/2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 69.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="sequence polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="sequence polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="sequence polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/protein_id="CAA34959.1"
/db_xref="G1:63595"
/db_xref="SWISS-PROT:P15720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="processing variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: GGMBP from: 1 to: 2256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318. .350
/note="splice variant"
892. .897
/note="polyA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2234. .2239
/note="polyA signal"
a 486 c 465 g
                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603.50
4.050
83.708
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US-09-218-277-12 x GGMBP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                            JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
authors do not rule out one gene for both proteins.
Location/Qualifiers
1. .1464
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
313 a 430 c 404 g 317 t
                                                                                                                                                                                                                                                                                                                                                                                                                          117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                                                                                                                                                                                    1 MetalaSerGlnLysargProSerGlnArgHisGlySerLysTyrLeual 17
                                                                                                                                                                                                                                                                                                                                                                                                      17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 ralaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
                                                                                                                                                                                                                                                                                                                                                                   25 ATGCCATCACAGAAGACCCTCACAGCGACACGGATCCAAGTACTTGGC 74
                                                                                                                                                                                             Gaps: 3
Percent Identity: 71.930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGMBP 2256 bp mRNA Chicken mRNA for myelln basic protein. X17103.1 GI:63594 myelln basic protein.
                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                   to: 1464
                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: RATMBP from: 1
                                                                                                                                                                         611.50
4.777
74.854
                                                                                                                                                                                                                                                alignment_block:
US-09-218-277-12 x RATMBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 CATAGCAAGACGC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 oMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chicken.
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ov:GGMBP
                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 G.....
                                                                                                                                                           alignment_scores
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SOURCE
ORGANISM
                                                                                     BASE COUNT
ORIGIN
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VERSION
                  FEATURES
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alignment_scores
                                                                                                                                                                                                                                                                                                                                                                              101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGR
FFSODRGAPKRGSGKVPWLKQSRSPLPSHARGRPGLCHMYKDSHTRTHYGSLPQKSQ
RTQDENPVVHFFKNIVTPPPPSQGKGRGLSLSRFSWGGRDSRSGSPLARR"
15 1 15 1 12 9 7 15 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNO132896 465 bp mRNA ROD 11-FEB-1999
Rattus norvegicus mRNA for myelin basic protein, 17 kDa isoform.
AJ132896. GI:4454312
Isoform: mbp gene; myelin; myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lobell, A.W.
Direct Submission
Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.

Rattus norvegicus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;

Eutheria: Rodentia; Sciurognathi; Muridae;

1 (bases 1 to 465)
                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                   116 rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaS 133
                                                                                                                                                                                                                                                                                                                                                          erAspTyrLysSerAlaHisLysGlyPheLysGlyVal.....AspAla 147
                                                                                                                                                                                                                                                                                                                                                                                           394 ATGAGCACAAATCTGCTCACAAGGGACACAAGGGATCCTATCACGAGGGC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 CAGGGCACTCTTTCCAAAATCTTTAAACTGGGAGGCTCTGGCTCCCGGCC 493
                                                                                         148 GlnGlyThrLeuSerLysIlePheLysLeuGlyGlyArg......
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh
                                                                                                                                                                                                                                                                                                                  347 CTGGGGTGGTGAAGGACACAAGCCGGGATACGGA...AGTGGAAAATTCT
                                                                      rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA
                                                                                                                                         83 spGluAsnProValValHisPhePheLysAsnIleValThrProArgThr
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/protein_id="CAA10805.1"
/db_xref="GI:4454313"

    .465
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Lewis rat"
/db_xref="taxon:10116"
1. .465
/gene="mbp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .465
/gene="mbp"
/note="17 kDa isoform"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 465)
Lobell, A.M. and Wigzell, H.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_ro:RNO132896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS RN0132896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
ACCESSION
VERSION
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ORIGIN
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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SOURCE
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                                                                    67
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420 ..... 420
                                                                                                                                                                    GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysGl 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
                                                                                                                                                                                                                                                                                                                         201 GAGCCCICTGCCTICTCAIGCCCGCAGCCGICCCGGGCTGTGCCACAIGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 aThralaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                               1 ATGGCATCACAGAGACCCTCACAGGGACACGGATCCAAGTACTTGGC 50
                                                                                                        1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                                                                                                                                                                                   Gaps: 4
Percent Identity: 62.437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGAAGAGACCCCCTGGATCTCCCATAGCAAGACGC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg
   Length:
                                                                                  to: 465
                                                                                  from: 1
                                                                                  Align seg 1/1 to: RN0132896
                                              alignment_block:
US-09-218-277-12 x RN0132896
588.50
4.598
64.975
  Quality:
Ratio:
                       Percent Similarity:
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Human filamin cDNA. Human f Fragment HG11775 of a new H Hybrid srmG/tylG OFF1. DNA i Platenolide synthase gene Platenolide synthase gene

8367 8630 13987 44377

104.08 118.61 201.72 718.21 718.21

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113.28
112.26
108.12
98.22
98.22
                                                                                                                                                                                                         T30269 standard, DNA, 516 1
T30269;
09-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 922.00
Ratio: 5.392
Percent Similarity: 100.000
    91.00
90.50
90.50
90.50
                                                                                                                                         seq_name: N_Geneseq_36:T30269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: T30269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-218-277-12 x T30269
                                                                                                                                                                                      documentation_block
  N_Geneseq_36:T73721
N_Geneseq_36:V23082
N_Geneseq_36:T80415
N_Geneseq_36:T7808
N_Geneseq_36:T780414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9616085-A1.
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                                                                                                                                                                                                              Len | Documentation ...

516 | Human myelin basic protein (decedible | Human myelin basic protein (MBF 516 | Human myelin basic protein (MBF 612 | Foetal myelin basic protein (MBF 612 | Foetal myelin basic protein MBF 612 | MMC chimera (MBP21.5-delta PLF 1155 | MM Chanera (MBP21.5-delta PLF 1155 | MM Chanera (delta PLP4 - MBP21.1147 | Encodeds RB35 protein from rat 621 | CDNA encoding soluble fused MHC 63 | Human BPP-PE chimeric protein cc 11700 | HMY-2 strain SB5 Contig ID 1702 | CDNA encoding soluble fused MHC 6225 | Human BPP-PE chimeric protein cc 11705 | HMY-2 strain SB5 Contig ID 1703 | HMY-2 strain SB5 Contig ID 1704 | Human adenosine Al receptor 1708 | MAIZE BX1 CDNA (DIMBOA blosynt 6225 | Human niterleukin-1 receptor 1700 | Total DNA sequence from cosmid 5001 | Total DNA sequence from cosmid 5001 | Total DNA sequence from cosmid 5002 | HSV L/ST region. Herpes Simpl 1113 | Calcium ion channel alphal sub 1711 | Human secreted protein 17 encoding Marmoset intracellular vitamin 679 | Human neuronal calcium channel 7791 | Human neuronal calcium channel
                                                                                                                                                                            software, version
       out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BSCOTE | 11.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00 | 10.00
                                                                                          About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 Orig ZSCORE 992.00 1389.40 899.00 1389.40 899.00 1383.28 899.00 1353.28 899.00 1353.28 899.00 1353.28 899.00 1353.28 899.00 1353.28 899.00 1353.28 899.00 1353.28 899.00 1346.53 134.00 1346.53 134.00 135.00 136.98 102.00 170.32 101.00 149.60 120.00 120.66 92.00 120.66 92.00 120.58 92.00 120.58 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 110.56 92.00 113.88
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Database sequences: 311585
Database length: 125096042
Search time (sec): 55.050000
                                               Date: Sep 26, 2000 8:19 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     information block:
US-09-218-277-12
OM of: US-09-218-277-12
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N_Geneseq_36:1730269
N_Geneseq_36:1732561
N_Geneseq_36:1741889
N_Geneseq_36:1741896
N_Geneseq_36:1741897
N_Geneseq_36:1741893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:T47123
N_Geneseq_36:T47123
N_Geneseq_36:T67171
N_Geneseq_36:T67181
N_Geneseq_36:T67169
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N_Geneseq_36:V68520
N_Geneseq_36:Y68520
N_Geneseq_36:V16305
N_Geneseq_36:V16305
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N_Geneseq_36:T41894
N_Geneseq_36:Q48976
N_Geneseq_36:Q48975
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N_Geneseq_36:084659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_36:T61016
N_Geneseq_36:X05110
N_Geneseq_36:V62149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geneseq_36:V29346
Geneseq_36:V43617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query: US-09-218-2
Query length: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                          -WAIT -THREADS=1
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POWER TO STATE THE PROPERTY OF THE PROPERTY OF
09-NOV-1996 (first entry)
Human myelin basic protein coding sequence.
Myelin basic protein; MBP; multiple sclerosis; MS; treatment;
prevention; analogue; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGCGTCACAGAAGAGACCCTCCCAGAGGCACGGATCCAAGTACCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= Myelin basic protein.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .516
/*tag= a
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51 CACAGCAAGTACCATGGACCATGCCAGGCATGGCTTCCTCCCAAGGCACA 100
 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human myelin basic protein (MBP) coding sequence.
Myelin basic protein; MBP; multiple sclerosls; MS; competition;
Inhibition; major histocompatability complex; MHC; thymocyte; T cell;
experimental allergic encephalomyelitis; EAE; analogue; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reatment of multiple sclerosis
Disclosure; Figure 1: 61pp; English.
Disclosure; Figure 1: 61pp; English.
Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive Tecal line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents.
The peptide analogues have a reduced susceptibility to proteolysis
pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                            LeuSerLysllePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
                                                                                                                                                        spTyrLysSerAlaH1sLysGlyPheLysGlyValAspAlaGlnGlyThr
                                                                                                                                                                                                                                                   84
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-1995; U14403.
18-NOV-1994; US-342408.
(NEUR-) NEUROCKINE BIOSCIENCES INC.
CONTON PJ. Gaur A, Ling N, Steinman L;
WPI; 96-266535/27.
P-PSDB; R99580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .516
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                               T32561 standard; DNA; 516 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:T32561
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Ratio: 5.392
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prevention; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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 101
                                       301
                                                                           117
                                                                                                                351
                                                                                                                                                      134
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                                                                                                                                                                                                                                                                     451
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34

1 MetalaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 1 ATGGCGTCACAGAAGAGACCCTCCCAGAGGCACGGATCCAAGTACCTGGC

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A cDMA sequence (T41899) codes for the native human 21.5 kDa foetal asoform (W00399) of myelin basic protein, WBP+X2Cy881/hum. This isoform (W00399) of myelin basic protein, WBP+X2Cy881/hum. This isoform includes an exon 2-encoded region (X2) that may contain an epitope involved in the pathogenesis of multiple sclerosis (KS); the X2 region is not found in the MBP of healthy adults. The CDNA can be obd. by PCR amplification (see also T42785-90) and used to produce recombinant MBP 21.5 in host, pref. bacterial, cells (see also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEE-1997 (first entry)

Human myelin basic protein (foetal isoform) cDNA.

Myelin basic protein; MBP; MBP+X2Cy881; proteolipid protein;

PLP; multiple sclerosis; autoimmune disease; diagnosis; therapy;

T-lymphocyte; T-cell; anergy; apoptosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller
                                                                   spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
                                                                                                                                                                                                                                                                                          ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
                                                                                                                                                                                                                                                                                                                                                                  pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                               ralaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTATAAATCGGCTCACAAGGGATTCAAGGGAGTCGATGCCCAGGGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1996.

22-ARY-1995; U05611.

02-MXY-1995; U5-431648.

02-MXY-1995; US-482114.

07-UN-1995; US-482114.

(ALEX.) ALEXION PHARM INC.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Lenardo MJ Matis L, McFarland HF, Mueller EE, Mu

Nye SH, Pelfrey CM, Squinto SP, Wilkins JA:

WPI: 96-505898/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T41889 standard; cDNA to mRNA; 594 T41889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:T41889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 OMEtAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 CATGGCTAGACGC 513
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10-FEB-1997 (first entry)
Foetal myelin basic protein MBP+X2Cys81/bact. DNA.
Myelin basic protein, MBP, MBP+X2Cys81, proteolipid protein, Imultiple sclerosis, autoimmune disease; diagnosis; therapy;
T-lymphocyte; T-cell; anergy; apoptosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGACTGTCCCTGAGCAGATTTAGCTGGGGGGCCGAAGGCCAGAGACCA 450
 polypeptides are useful
1 treatment of MS.
14 C; 171 G; 96 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
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                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                              GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 CAGAAGICACACGGCCGGACCCAAGAIGAAAACCCCGIAGICACITCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCCGTCACAGAAGACCTCCCCAGAGGCACCGGATCCAAGTACCTGGC
                                                                                                                                                                                                                        17 aThralaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA
                                                                                                                                                                                                                                                                    34 rgAspThrGlylleLeuAspSerIleGlyArgPhePheGlyGlyAspArg
                                                                                                                                                                                                                                                                                             GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAGG
                                                                                                                                                                                                                                                                                                                               yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG
                                                                                                                                                                           1 MetalaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                                                                                                                                                                                                                                                                                                                       201 GAGCCCTCTCCTCTCATGCCCGCAGCCAGCCTGGGCTGTGCAACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGl
                                                                                                                                                                                                                                                                                                                  GlyAlaProLysArgGlySerGly......
                                                                                         Percent Identity: 86.802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGAAGAGATAGTCGCTCTGGATCACCCATGGCTAGACGC
                                                                      Length:
Gaps:
T41896-97). Recombinant MBP 21.5 polyr
clinical assessment, diagnosis and tre
Sequence 594 BP; 143 A; 184 C;
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ID T41896 standard; DNA; 612
AC T41896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_name: N_Geneseg_36:T41896
                                                                   899.00
5.257
86.802
                                                                                                                alignment_block:
US-09-218-277-12 x T41889
                                                                                                                                                    Align seg 1/1 to: T41889
                                                                    Quality:
Ratio:
                                                                                          Percent Similarity:
                                                           alignment_scores:
                                                                                                                                                                                                                                               21
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Disclosure; Page 81-82; 156pp; English.
A DNA sequence (T41896) codes for the human 21.5 kDa foetal isoform (W06107) of myelin basic protein, MBPA-X2CygSAI/bact., and utilises bacterially-preferred codons in place of the native human codons (see also T41889). This increases prodn. of the MBP in E. coli by at least 5%. Recombinant MBP 21.5 polypeptides (see also W00399 and W06108) are useful in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                             protein variant(s)
                                                                                                                          Ę,
                                                                                                                                                                                                           used in the assessment, diagnosis and treatment of multiple
                                                                                                                        Mueller
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Percent Identity: 86.802
                                                                                                                          EE,
07-000-1996.
22-ARR-1996; U5-611.
22-ARR-1995; U5-431644.
02-MAY-1995; U5-431644.
07-UNN-1995; U5-482114.
(ALEX-) ALEXION PHARM INC.
(USH) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McParland HF, Mueller EE, Nye SH, Pelfrey CM, Squinto SP, Wilkins JA; WPI, 96-5059987.
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                                                                                                                                                                                      New human myelin basic protein and proteolipid
                                                                                                                                                                                                                                                                                                                                                                                 166
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5.257
86.802
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US-09-218-277-12
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seq_documentation_block:
ID T41893 standard; DNA; 1122 BP.
AC T41893;
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WO9634622-A1.
07-NOV-1996.
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D 07-NOV-1996.
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D 07-NOV-1996.
D 08-MAY-1995; US-431644.
D 07-NOV-1996.
D 08-MAY-1995; US-43114.
D 08-MAY-1995; US-43114.

A LEEX ) ALEXION PHARM INC.
A (USSH) US DEPT HEALTH & HUMAN SERVICES.
A (USSH) US DEPT HEALTH & HUMAN SERVICES.
D NAPIS B 05-505898/50.
D 08-SDB; W06108.
D 08-SDB; W06108.
D 08-MUMAN myelin basic protein and proteolipid protein variant(s) rused in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A DNA sequence (T41897) codes for the human 21.5 kDa foetal isoform (W06108) of myelin basic protein, MBP+X28erBl/Dact., and utilises codons that are preferentially used in highly-expressed bacterial genes and includes a sequence coding for an N-terminal haxahistidine tag. This facilitates large-scale prodn. and purification of MBP 21.5 polypeptides (see also W00399 and W06107) are useful in the clinical assessment, diagnosis and treatment of MS. Sequence 612 BP; 117 A; 215 C; 166 G; 114 T;
                                                                                                                                                                                                                                                                                     01-FEB-1997 (first entry)
Foetal myelin basic protein MBP+X2Ser81/bact.
Whelin basic protein; MBP; MBP+X2Ser91; proteolipid protein; PLP; multiple sclerosis; autoimmune disease; diagnosis; therapy; T-lymphocyte; T-cell; anergy; apoptosis; ds.
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                                                                                           125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGl
                                    451 GCCTTCGGTTACGGCGGCGCGTGCGTCCGACTATAAATCTGCTCACAAAGG
                                                                       141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 899.00 Length: 197
Ratio: 5.257 Gaps: 1
nilarity: 86.802 Percent Identity: 86.802
                                                                                                                                               158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                  Align seg 1/1 to: T41897 from: 1 to: 612
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ID T41897 standard; DNA; 612 BP.
AC T41897;
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US-09-218-277-12 x T41897
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sclerosis

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Sclenosis

Sclenosis

Sclenosis

Claim 46; Page 110-112; 156pp; English.

Calm 67; See also W0039) and delta PLP4 (W06101), a proteollipid protein (PLP) mutein that lacks all 4 hydrophobic domains of protein (PLP) mutein that lacks all 4 hydrophobic domains of protein (PLP) mutein that lacks all 4 hydrophobic domains of mative human PLP (W06106) but includes PLP epitoppes associated with cultiple sclerosis (MS). It was constructed from DNA sequences condity MBP21.5 (T41889) and delta PLP4 (T41891). The gene fusion control pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 in E. coli Wallo (DE3).

Calm vector pET22b was used to express MP4 (T41891). The gene fusion be used in the clinical assessment, diagnosis and treatment of MS.
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MP4 chimera (MBP21.5-delta PLP4 fusion) DNA.
Proteolipid protein: PLP; delta PLP4; myelin basic protein; 1
MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; therapy; T-lymphocyte; T-cell; MP4 chimera; ds.
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GGTGCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCG
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C2-MAY-1995; US-431648.
C2-MAY-1995; US-431644.
C7-MAY-1995; US-482114.
C7-MAY-1995; US-482114.
C7-MAY-1995; US-482114.
C1-MAY-1995; US-482114.
C1-MAY-1995; US-482114.
C1-MAY-1995; US-482114.
C1-MAY-196-50598/50.
C1-MAY
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01-FEB-1997 (first entry)
MP3 chimera (MBP21.5-delta PLP3 fusion) DNA.
Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
MBP21.5; multiple solerosis; autoimmune disease; diagnosis;
therapy; T-lymphocyte; T-cell; MP3 chimera; ds.
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                                                                                                                                        1 ATGGCGTCTCAGAAACGTCCGTCCAGCGTCACGGCTCCAAATACCTGGC
                                                                                                                                                                      51 CACCGCCAGCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACC
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                                                                                                                                                                                                                                                                                                     201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGT
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Percent Identity: 86.802
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ID T41892 standard; DNA; 1155 BP
                          899.00
5.257
86.802
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                                                                                                Align seg 1/1 to: T41893
                                                                  alignment_block:
US-09-218-277-12 x T41893
                             Quality:
Ratio:
                                              Percent Similarity:
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WO9634622-A1
                    alignment_scores
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Taim 45; Page 108-110; 155pp; English.

A DNA construct (T41882) codes for MP3 chimera (W06102), a fusion protein composed of human myells basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and delta PLP3 (W00400), a proteolipid protein (PLP) mutein that lacks hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (WS). It was constructed from DNA sequences encoding MBP21.5 (T41889) and delta PLP3 (T41890). The gene fusion in vector PET22b was used to express MP3 in E. coli W110 (DB3). PLP polypeptides (see also W00400, W061010 and W06103-05) can be used in the clinical assessment, diagnosis and treatment of MS. Sequence 1155 BP; 239 A; 363 C; 306 G; 247 T;
                                                                                                                                                                                          New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple
                                                                                                               Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eLysAsnileValThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GGTGCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 1
Percent Identity: 86.802
                                                                                                               EE,
02-MX-1995; US-431648.
02-MX-1995; US-431644.
07-UUN-1995; US-482114.
(ALEX-) ALEXION PHARM INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McParland HF, Mueller EE, Nye SH, Pelfrey CM, Squinto SP, Wilkins JA; WPI; 96-505898/20.
P-PSDB; W06102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GlyAlaProLysArgGlySerGly......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T41892 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899.00
5.257
86.802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-218-277-12 x T41892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores;
                                                                                                                                                                                                                                           sclerosis
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501

125

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GGTGCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCG 200
                                                                                                             GlyAlaProLysArgGlySerGly......
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P-PSDB; W06104.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T41894;
                                                         101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 48; Page 115-117; 156pp; English.

C A DNA construct (T41895) codes for MMOGP4 chimera (W06105), a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin protein composed of human myelin takes also w00399), the extracellular domain of human myelin coligodendrocyte glycoprotein (W06) and delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lacks all 4 hydrophobic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). It was constructed by inserting a sequence encoding the MOG molety into MP4 chimera DNA (see also T41893) between the MBP and PLP derived sequences. The recombinant MMOGP4 chimera can be expressed in bacterial cell hosts. PLP polypeptides (see also W00400 W06101-03 and W06105) are useful in the clinical assessment, diagnosis and treatment of MS. Sequence 1476 BP; 332 A; 434 C; 403 G; 307 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F 02-APR-1995. US-431648.

R 02-MAY-1995; US-431648.

R 02-MAY-1995; US-431648.

R 07-UN-1995; US-43164.

A (ALEX.) ALEXION PHARM INC.

A (USSH ) US DEPT HEALTH & HUMAN SERVICES.

I Lenardo MJ, Matis L, Maraland HF, Mueller EE, Mueller JP; Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

W WPI; 96-505898/70.

R PPEDB; W06105.

R PPEDB; W06105.

T used in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (first entry)
MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion) DNA.
Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
therapy; T-lymphocyte; T-cell; MMOGP4 chimera;
myelin oligodendrocyte glycoprotein; MOG; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetalaSerGlnLygArgProSerGlnArgHisGlySerLysTyrLeuAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                             1 ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC
                               451 GGCTTCGGTTACGGCGCCGTCCGACTATAAATCTGCTCAAAAGG
                                                                                                             141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG
  GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 1
Percent Identity: 86.802
                                                                                                                                                                                                                     158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: T41895 from: 1 to: 1476
                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
T41895 standard; DNA; 1476 BP.
T41895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.257
                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:T41895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        899.00
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US-09-218-277-12 x T41895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity
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WO9634622-A1.
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Claim 47; Page 113-114; 156pp; English.

DNR construct (141894) codes for PM4 chimera (W06104), a fusion protein composed of delta PLP4 (W060101) and MBP21.5 (W00399).

Delta PLP4 is a proteolipid protein (PLP) mutein that lacks all 4 hydrophobat domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (first entry)
PM4 chimera (delta PLP4-MBP21.5 fusion) DNA.
Protecolipid protein; PLP, delta PLP4; myelin basic protein;
MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
therapy; Tlymphocyte; T-cell; PM4 chimera; ds.
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                                                                                                                                                                                                                                                             500
                                                                                                                                                    350
                                                                                                                                                                                       eLysasnilevalThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                      550
 250
                                                                                                                                                                                                                                                                                                                                                                                                                 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
                                      74
                                                                                                                 91
                                                          GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh
                                                                                                                                GGCTTCGGTTACGGCGGCCGTCCGACTATAAATCTGCTCACAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 CTTCAAAGGCGTGGATGCCCAGGGTACCTTGTCCAAATTTTCAAACTGG
TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGT
                                      .. LysAspSerHisH1sProAlaArgThrAlaH1sTyrGlySerLeuPro
                                                                                                                                                                                                                          351 CAAAACATTGTGACCCCGCGTACCCCGCCGCCGTCTCAGGGCAAAGGCC
                                                                                                                                                                                                                                                                                                                                         GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaH1sLysG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-RR-1996; U05611.
02-MAY-1995; U5-431648.
02-MAY-1995; U5-431644.
02-MAY-1995; U5-431644.
(ALEX-) ALEXION PHARM INC.
(ALEX-) NG DEPT HEALTH & HUWAN SERVICES.
LOGATO MJ, MATIS L, MCFARLAND HF, MUELLER INVE SH, Pelfrey CM, Squinto SP, Wilkins JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID T41894 standard; DNA; 1125 BP
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RB35 antigen; immunogen; myelin; rat; brain; antibody; IgG1; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MS. The DNA was constructed from sequences encoding delta PLP4 (T41891) and MBP21.5 (T41889). The gene fusion can be used to express PM4 in bacterial hosts. PLP polypeptides (see also W00400, W06101-03 and W06105) can be used in the clinical assessment, diagnosis and treatment of MS. 359 C; 299 G; 228 T; Sequence 1125 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1020 CAAAGGCGTGGATGCCCAGGGCACCCTGTCCAAAATTTTCAAACTGGGCG 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 TTCGGCTACGGCGGCGTGCGTCCGACTATAAATCTGCTCACAAAGGCTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 PheGlyTyrGlyGlyArgAlaSerAspTyrLySerAlaH1sLysGlyPh 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 eLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyG 159
                                                                                                                                                                                                                                        720 CCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGTACA 769
                                                                                                                                                                                                                                                                                                                           52 AlaProLysArgGlySerGly......58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 LysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePheLy 92
                                                                                                                                                                                                                                                                                                                                                                                                                  59 ysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuProGln 75
                                                                                               Length: 196
Gaps: 1
Percent Identity: 86.735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T41894 from: 1 to: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-1994 (first entry)
Nucleotides 301-1464 of rat myelin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID 048976 standard; cDNA to mRNA; 1164 BP.
AC 048976;
                                                                                               894.00
5.259
86.735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:Q48976
                                                                                                                                                   US-09-218-277-12 x T41894
                                                                                    alignment_scores:
Quality:
Ratio:
                                                                                                                     Percent Similarity:
                                                                                                                                           alignment_block:
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7. Torner 1992; 055983.

7. FEB-1992; 055983.

7. FEB-1992; 055983.

7. TOKE ) TOSHIBA KK.

8. WPI; 93-308342/39.

7. TOKE ) TOSHIBA KK.

8. WPI; 93-308342/39.

7. Toke ) Torner in the proteins distributed in the brain antibody against the proteins distributed in the brain and conclonal antibody against the proteins distributed in the brain spread. By using rat brain extract as immunogen belonging to risp pread 2.3; 16pp; Japanese.

7. Totalm 2; Page 2-3; 16pp; Japanese.

8. Claim 2; Page 2-3; 16pp; Japanese.

8. Claim 2; Page 2-3; 16pp; Japanese.

9. Claim 2; Page 2-3; Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1993.
07-FEB-1992; 055983.
07-FEB-1992; DP-055983.
(TOKE ) TOSHIBA KK.
WPI; 93-308342/39.
Monoclonal antibody against the proteins distributed in the brain - is prepd. by using rat brain extract as immunogen belonging to IgG class which combines to rat brain extract antigen Claim 2; Page 2-3; 16pp; Japanese.
The sequence coding for RB35 was isolated from a CDNA library prepared from total adult female Sprague-Dawley rat brain mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1994 (first entry)
Encodes RB35 protein from rat brain.
RB35 antigen; immunogen; myelin; Sprague-Dawley; rat; brain;
antibody; IgG1; da
Rattus norvegicus (Sprague-Dawley).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 AspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSe 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 lyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyVal 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ThrProArgThrProProProSerGlnGlyLysGlyArgGlyLeuSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACACCTGGTACACCCCCTCCATCCCAAGGAAAGGGGAGAGGCCTGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CAGCAGATTTAGCTGG.............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 76
Gaps: 1
Percent Identity: 46.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q48976 from: 1 to: 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q48975 standard; cDNA to mRNA; 1147 BP. Q48975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 rArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 CCGCTCTGGATCTCCCATAGCAAGACGC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 160.00
Ratio: 4.444
Percent Similarity: 47.368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q48975
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US-09-218-277-12 x Q48976
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Rattus norvegicus. J05219982-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J05219982-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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effect on non-target cells.
  8888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel fused major histocompatibility complex:antigenic peptide complex - useful to induce tolerance to an autoantigen-related classase e.g. insulin-dependent diabetes mellitus
Example 1; Pages 118-119; 142pp; English.

The present sequence encodes a novel soluble fused major histocompatibility complex (MHC) heterodimer:peptide complex comprising 1st and 2nd MHC domains, linked by a 5.25 residue linker, and an antigenic peptide able to associate with a peptide binding groove of the MHC molecule, linked in frame to the 2nd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1997 (first entry)

CDNA encoding soluble fused MHC heterodimer:peptide complex pLJ13.

Soluble, fusion; major histocompatibility complex; MHC;
heterodimer; complex; antigen; binding groove; tolerance;
autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
antagonist; T cell; anergy; presenting cell; ds.
RB35 is used as an immunogen to generate monoclonal antibodies of the IgG1 subtype which specifically bind to a protein in rat brain extract of mol.wt. ca. 30 kD. 331 C; 329 G; 226 T; Sequence 1147 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheppard PO;
                                                                                                                                                                                                                                                                                                   1093 G...... 1093
                                                                                                                                                                                                                                  1143 CCTCCATCCCAAGGAAAGGGGAGAGGCCTGTCCCTCAGCAGATTAGCTG 1094
                                                                                                                                                                                                                                                                                                                                                                                                101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
                                                                                                                                                                                                                                                                                                                            134 spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
                                                                                                                                                                                                                                                                        117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                                                                                                                                                                                                                                  151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
                                                                                           Gaps: 71 Gaps: 1 Percent Identity: 43.662
                                                                                                                                                                                           Align seg 1/1 to reverse of: Q48975 from: 1 to: 1147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T47123 standard; cDNA; 621 BP. T47123;
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/*tag= a
                                                                                                                                                                US-09-218-277-12 x Q48975/rev
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                                                                                              135.00
4.355
43.662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995; US-482133.
07-JUN-1995; US-480002.
07-JUN-1995; US-483241.
27-OCT-1995; US-005964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      167 oMetalaArgArg 171
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07-JUN-1996; U10102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block
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WPI; 97-052337/05.
P-PSDB; W10493.
                                                                                               Quality:
                                                                                                         Ratio:
Percent Similarity:
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                                                                                 alignment_scores:
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                                                                                                                                                   alignment_block
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Merical Description of auto: immune diseases, particularly used for the treatment of auto: immune diseases, particularly used for the treatment of auto: immune diseases, particularly multiple sclerosis

multiple sclerosis

Claim 7: Page 22: 54pp; English.

Se chimeric proteins have been developed comprising a Pseudomonas acruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)

moiety selected from: (a) MBP; (b) amino acids 69:88 of guinea-ply MBP or an antigenic portion; (c) amino acids 69:88 of guinea-ply MBP or an antigenic portion; (d) amino acids 143:168 of human MBP or an antigenic portion; (d) amino acids 143:168 of human MBP or an antigenic portion; (d) amino acids sequence in which one or more amino acids sequences of (a), (b), (c), or (d), the modified sequences retaining at least 75% homology with the amino acid sequences. The present sequence represents an oligonuclectide used for constructing human BPP-PE chimeric proteins. The chimeric proteins can be used for the treatment of autoimmune diseases such as multiple sclerosis. The chimeric proteins of action the paying no acide of the construction for the treatment of autoimmune diseases such as multiple sclerosis. The chimeric proteins of action the paying no acide of the construction for the paying no acide of the construction for the
domain by a 5-25 residue linker. The complex can be used to induce immunological tolerance in adults susceptible to, or suffering from an autoantigen related disease, e.g. insulin dependent diabetes mellitus (IDDM), by antagonising the binding of particular T cells and antigen presenting cells, to induce anergy (immunological non-responsiveness) in the targeted T cell. As the heterodimers and corresponding antigen are permanently linked into a single chain, obstating the requirement for complex heterodimer truncation of formation, the complex eliminates inefficient and non-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-FEB-1998 (first entry)
Human BPP-PE chimeric protein construction oligonucleotide Oligo 3.
Pseudomonas exotoxin; myelin basic protein; chimeric protein; autoimmune disease; multiple sclerosis; human; ss.
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17-NOV-1996; IL0151.
17-NOV-1995; IL-116044.
17-NOV-1995; IL-116044.
(YISS ) YISSUM RES & DEV CO.
Beraud E, Lorberboum-Galaki H, Marianovsky I, Steinberger I;
Yarkoni S;
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Ratio: 4.786 Gaps: 1
Percent Similarity: 75.676 Percent Identity: 72.973
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ID T67170 standard; DNA; 63 BP.
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US-09-218-277-12 x T47123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide loading.
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WO9719179-A1.
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Yarkon1 S;
WPI: 97-298116/27
WPI: 97-2980domonase exotoxin-myelin basic protein chimeric proteins used for the treatment of auto:immune diseases, particularly multiple sclerosis
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17-NOV-1996; IL0151.
26-DEC-1995; IL-116559.
17-NOV-1995; IL-116044.
(YISS ) YISSUM RES & DEV CO.
Beraud E, Lorberboum-Galski H, Marianovsky I, Steinberger I;
                                                                                                                                                                                                                                                                                                                                19-FEB-1998 (first entry)
BPP-PE chimeric protein synthesis oligonucleotide Oligo 3.
Pseudomonas exotoxin; myelin basic protein; chimeric protein; autoimmune disease; multiple sclerosis; human; ss.
  167168 standard; DNA; 63 BP.
                                                                                                                                                                                                 seq_name: N_Geneseq_36:T67168
                                                                                                                                                                                                                                                        documentation_block:
                                                                                   99 rProPro 101
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WHEN PSEUGOMORIAS exotoxin-myelin basic protein chimeric proteins used for the treatment of auto:immune diseases, particularly used for the treatment of auto:immune diseases, particularly nultiple sclerosis

The sclerosis control of the sclerosis of the treatment of the schimeric proteins of the sclerosis o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-FEB-1998 (first entry)
Human BPP-PE chimeric protein construction oligonucleotide Oligo 5.
Pseudomonas exotoxin; myelin basic protein; chimeric protein;
autoimmune disease; multiple sclerosis; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lorberboum-Galski H, Marianovsky I, Steinberger I;
                                                                                                                                                                                                                                                                                                                                                             83 AspGluAsnProValValHisPhePheLysAsnIleValThrProArgTh
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Gaps: 0
Percent Identlty: 100.000
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Gaps: 0
Percent Identity: 100.000
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17-NOV-1996: IL0151.
26-DEC-1995: IL-116659.
(YISS ) YISSUM RES & DEV CO.
Beraud E, Lorberboum-Galski H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T67171 standard; DNA; 63 BP.
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                                                                                                        Quality: 107.00
Ratio: 5.632
Percent Similarity: 100.000
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Ratio: 5.632
Percent Similarity: 100.000
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21
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US-09-218-277-12 x T67170
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US-09-218-277-12 x T67171
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WPI; 97-298116/27.
BP;
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WO9719179-A1.
63
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                                                                                   alignment_scores:
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Claim 7; Page 9; Supp; English.

New chimeric proteins have been developed comprising a Pseudomonas aerotoxin (PE) modety linked to a myelin basic protein (MBP)

moiety selected from: (B) MBP; (D) amino acids 69-88 of guinea-pig MBP or an antigenic portion; (G) amino acids 84-102 of human MBP or an antigenic portion; (A) amino acids 143-168 of human MBP or an antigenic portion; (A) amino acids sequence in which one or more amino acids have been deleted, added, substituted or mutated in the amino acid sequences of (a), (b), (c), or (d), the modified sequences retaining at least 75% homology with the amino acid sequences. The present sequence represents an oligonuclectide used in the synthesis of BPP-PE chimeric proteins can be used for the treatment of autoimmune diseases such as multiple sclerosis. The chimeric proteins can specifically target and kill MBP specific T cells while having no effect on non-target cells.

Sequence 63 BP; 21 A; 15 C; 8 G; 19 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 19
Gaps: 0
Percent Identity: 100.000
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Percent Similarity: 100.000
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83 AspGluAsnProValValHisPhePheLysAsnIleValThrProArgTh 99

Align seg 1/1 to: T67171 from: 1 to: 63

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7 Sequence (Sign1_7) prodata/1/lna/Sp_COMB. seq:US-08-78:1122-1 + 922:00 1580.75 1.5e-80 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1539.74 2.8e-78 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1539.44 3.0e-78 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1533.14 6.4e-78 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1533.17 6.6e-78 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1530.17 5.0e-79 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1530.17 5.0e-79 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-2 + 899:00 1530.17 5.0e-79 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-5 - 25:00 412.50 7.5e-10 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-6 - 162:00 375:73 1.9e-13 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-6 - 162:00 375:73 1.9e-13 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-6 - 162:00 281:35 2.1e-08 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-6 - 162:00 281:35 2.1e-08 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-6 - 162:00 281:35 2.1e-08 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-7 - 135:00 281:55 2.1e-08 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-7 - 135:00 281:55 2.1e-08 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-7 - 135:00 281:55 8.5e-06 (1901.7) prodata/1/lna/Sp_COMB. seq:PCT-US96-05511A-7 - 1001 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:93 891:00 121:85 26:9
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Database length: 68777915
Search time (sec): 46.89000
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Database: Issued_Patents_NA:*
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-(2-/cgn1_1/USPTO_spco1/US09218277/runat_26092000_140043_3811/app_query.fasta_1.231
-DB-ISSUGG_Patents_NA -GEMT-fastap -SUFFIX-rni -GAPOP=12_000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -UOOPEXT-0.000
-GAPEXT-4.000 -GAPEXT-0.050 -XGAPOP=10.000 -XGAPEXT-0.500
-FGAPOP=6.000 -GAPEXT-7.000 -YGAPOP=10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -XGAPOP=10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -XGAPOP=10.000 -YGAPEXT-0.500
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTEMT-pfs
-NORM-ext -MINLEN-0 -NAXIEN-200000000
-USER-US09218277_@CGN1_1_57 -NCEU-6 -ICPU-3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8e-11
2.1e-08
8.5e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5e-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           668 1
8367 1
8367 1
8367 1
13987
44377 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-218-277-12 x US-08-781-122-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-781-122-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgnl_7/ptodata/1/1na/5B_COMB_seq:US-08-394-326-1 + /cgnl_7/ptodata/1/1na/5B_COMB_seq:US-08-394-326-11-1/cgnl_7/ptodata/1/1na/5C_COMB_seq:US-08-216-260-3 - /cgnl_7/ptodata/1/1na/5A_COMB_seq:US-08-331-004A-1 - /cgnl_7/ptodata/1/1na/5A_COMB_seq:US-08-331-004A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 922.00
Ratio: 5.392
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-781-122-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: - 2
           34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg
                                                                                                                                                              17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Colu
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                           1 ATGGCGTCACAGAAGACCCTCCCAGAGGCACGGATCCAAGTACCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                           MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                                                      CACAGCAAGTACCATGGACCATGCCAGGCATGGCTTCCTCCCAAGGCACA
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Percent Identity: 100.000

ţ O: 516

34

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50 100

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COMPOUTER: IBM POTEST
COMPOUTER: IBM POTEST
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
EURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,122
FILING DATE: 09-JAN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REJESTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 690068.418C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENDOME: GARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
; Sequence 1, Application US/08781122
; Patent No. 5948764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn1_7/ptodata/1/ina/5D_COMB.seq:US-08-781-122-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gaur, Amitabh
APPLICANT: Conlon, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ling, Nicholas
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR TREATMENT OF MULTIPLE UTILIZING PEPTIDE ANALOGUES OF HUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 Fifth Avenue
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lenardo. Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Applicati
GENERAL INFORMATION:
APPLICANT: Muelle
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
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STREET: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Maurice M. Klee
1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Lenardo. Michael J.
McFarland, Henry F.
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TOPOLOGY: Linear

MOLECULE TYPE: CDNA to mRNA

DESCRIPTION: Human 18.5 kDa form of MBP
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: ALX-
REFERENCE_DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEPAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGIH: 519 base pairs
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: PCT-US96-05611A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-218-277-12 x PCT-US96-05611A-4
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                                                                             151
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                                                                                                                                                                                                                                                                   304 CCCCCGTCGCAGGGAAAGGGGAGAGGACTGTCCCTGAGCAGATTTAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 CACAGCAAGTACCATGGACCATGCCAGGCATGGCTTCCTCCCAAGGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                        GGGGCCGAAGGCCAGAGACCAGGATTTGGCTACGGAGGCAGAGCGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                         rAlaH1STyrGlySerLeuProGlnLysSerH1SGlyArgThrGlnAspG
                                                           LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
oMetAlaArgArg 171
                                                                                                                                    spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||||||||||||||||
                                                                                                                                                                                                                                                                                       ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTCACTATGGCTCCCTGCCCCAGAAGTCACACGGCCGGACCCAAGATG
                                       CTTTCCAAAATTTTTAAGCTGGGAGGAAGAGATAGTCGCTCTGGATCACC
                                                                                                                                                                                                             pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCGCCAAAGCGGGGCTCTGGCAAGGACTCACACCACCGGCAAGAAC
                                                                                                                ACTATAAATCGGCTCACAAGGGATTCAAGGGAGTCGATGCCCAGGGCACG
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5.392
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CATGGCTAGACGC 516

seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-1

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Sequence 1, Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Lenardo. Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
PCT-US96-05611A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 0,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
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OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: Roth, H. J.
AUTHORS: Kronquist, K. E.
AUTHORS: Kerlero de Rosbo, N.
AUTHORS: Crandall, B. F.
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MBP+X2Cys81/hum. (Human 21.5 kD
DESCRIPTION: of MBP)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US96/05611A FILING DATE: 02-MAY-1995 CLASSIFICATION:
                         VOLUME: 1/
TACES: 312 - 328
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                                                                                JOURNAL:
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: USA
                                                                                  cDNA Cloning Journal of Neuroscience Research
                                                                                                                      : Crandall, B. F.
: Campagnoni, A. T.
Evidence for the Expression of Four
Myelin Basic Protein Variants in the
Developing Human Spinal Cord Through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pelfrey, Clara M.
Squinto, Stephen P.
Wilkins, James A.
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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-1
                                   seq_documentation_block:
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                                                                  seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-2
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 GAGGAAGAGATAGTCGCTCTGGATCACCCATGGCTAGACGC
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                                                                                                                                                                          401 GAGGACTGTCCCTGAGCAGATTTAGCTGGGGGGCCGAAGGCCAGAGACCA
                                                                                                                                                                                                                                                                                                                                           108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
                                                                                                                                                                                                                                                                                                                                                                                               351 CAAGAACATTGTGACGCCTCGCACACCACCCCGTCGCAGGGAAAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CAGAAGTCACACGGCCGGACCCAAGATGAAAACCCCGTAGTCCACTTCTT
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                                                                                                                          lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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Ratio:
                Application PC/TUS9605611A
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5.257
86.802
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.

APPLICANT:

Mueller, Eileen Elliott Nye, Steven H. Pelfrey, Clara M. Squinto, Stephen P.

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REFERENCE/DOKET NUMBER: ALX-129
REFERENCE/DOKET NUMBER: ALX-129
REFERENCE: 255 1400
RELEFAX: (203) 254 1101
RELEFAX: (203) 255 125 125
RELEFAX: (203) 255 12
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US-09-218-277-12 x PCT-US96-05611A-2
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Percent Similarity:
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APPLICATION NUMBER: 08/431,644
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1951 Bus
CITY: Fairfield
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                  CACCGCCAGCACCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC
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5.257
86.802
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ER: ALX-129
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Percent Identity: 86.802
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seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-3
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                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: MacIntosh Centris 610
OPERATING SYSTEM: System 7
SOTTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: JUNE 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Nye, Steven H.
APPLICANT: Pelirey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 GCGGCCGTGATAGCCGTTCTGGCTCTCCGATGGCTAGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 CTTCAAAGGCGTGGATGCCCAGGGTACCTTGTCCAAAATTTTCAAACTGG
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                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U:
ZIP: 06430
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STATE: Connecticut
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Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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REFERENCE/DOCKET NUMBER: ALX-129

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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-3
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEPAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA to mRNA DESCRIPTION: MBP+X2Ser81/bact. HYPOTHETICAL: NO
                                                                                                                                                                                                                                                          151
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: Nucleic acid
                   158
                                                                                      141
                                                                                                                        451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CACCGCCAGCACCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACC 100
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                                                                                                                                                                                                                                                                                                                             ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC 50
lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                              ...LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
                                                                      yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
                                                                                                                                         GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGl 141
                                                                                                                                                                                                             rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
                                                                                                                                                                                         GTGGCCTGTCCCTGAGCCGTTTCAGCTGGGGCGCCGAAGGCCAGCGTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCG 200
                                                  CTTCAAAGGCGTGGATGCCCAGGGTACCTTGTCCAAAATTTTCAAACTGG
                                                                                                                     GGCTTCGGTTACGGCGGCCGTGCGTCCGACTATAAATCTGCTCACAAAGG
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5.257
86.802
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; MOLECULE TYPE: Other nucleic DESCRIPTION: MP4 chimera; HYPOTHETICAL: NO ANTI-SENSE: NO PCT-US96-05611A-26
                                alignment_block:
US-09-218-277-12 x PCT-US96-05611A-26
                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-26
 Align seg 1/1
                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application PC/TUS9605611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (203) 255
TELEFAX: (203) 254 11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MONINGER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: ALTELECOMMUNICATION INFORMATION: TELEPHONE: (203) 255 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft WO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 GCGGCCGTGATAGCCGTTCTGGCTCTCCGATGGCTAGACGT
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COMPUTER: Macluco...

OPERATING SYSTEM: System 7

OPERATING SYSTEM: TATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/05611A FILING DATE: 02-MAY-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                               STRANDEDNESS: Double TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                             TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Klee, Maurice M. REGISTRATION NUMBER: 30,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1951 Burr Street CITY: Fairfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 0.8 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                       Quality:
                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Connecticut
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Squinto, Stephen P.
Wikkins, James A.
WINTION: Modified Myelin Protein Molecules
EDOUENCES: 29
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Matis, Louis A.
Mueller "'
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SYSTEM: System:
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Nye, Steven H.
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 PCT-US96-05611A-26
                                                                                     899.00
5.257
86.802
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254 1101
MO: 26:
                                                                                       Percent
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                                                                                     Gaps:
Identity:
 from: 1
                                                                                                                       Length:
to: 1122
                                                                                       86.802
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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-25
                                                                                                                  APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application PC/TUS9605611A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 0.8 Mb storage
COMPUTER: MacIntosh Centris 610
OPERATING SYSTEM: System 7
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                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTTCGGTTACGGCCGCCGTGCGTCCGACTATAAATCTGCTCACAAAGG 500
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                                                                                  06430
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Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                     USA
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; TOPOLOGY: Linear nucle; MOLECULE TYPE: Other nucle; DESCRIPTION: MP3 chimera; HYPOTHETICAL: No; ANTI-SENSE: NO PCT-US96-05611A-25
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US-09-218-277-12 x PCT-US96-05611A-25
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US96/0561
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 03,399
REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: A1,399
REFERENCE,DOCKET NUMBER: A1,399
REFERENCE, A1,399
REFERENCE,DOCKET NUMBER: A1,399
REFERENCE,DOCKET NUMBER: A1,399
REFERENCE,DOCKET NUMBER: A1,399

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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                  301 CAGAAATCCCACGGCCGTACCCAGGATGAAAACCCGGTGGTGCACTTCTT 350
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351 CAAAAACATTGTGACCCCGCGTACCCCGCCGCCGTCTCAGGGCAAAGGCC
                                                                                                                                                                                          75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CACCGCCAGCACCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
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                                        eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTGCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCG
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02-MAY-1995
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5.257
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seq_name: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-28
                                                                                                                                                                                                                           APPLICATION NUMBER: 08/431,644
FILING DATE: May 2,1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2,1995
APPLICATION NUMBER: 08/482,114
FILING DATE: May 7,1995
AFICTORIES JUNE 7,1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, MAULICE M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           equence 28, Application PC/TUS9605611A GENERAL INFORMATION: APPLICANT: Mueller, John P.
                                                                                                            TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1476 base pairs
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
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APPLICANT:
APPLICANT:
APPLICANT:
              MOLECULE TYPE: Other nucleic acid DESCRIPTION: MMOGP4 chimera HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: MICTOSOFT WORD 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                           STRANDEDNESS: DOI TOPOLOGY: Linear
                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                 (203)
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                                                                                                Double
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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-28
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               158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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                                                                         yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG
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GCGGCCGTGATAGCCGTTCTGGCTCTCCGATGGCTAGACGT 591
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5.257
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seq_documentation_block:

Sequence 27, Application PC/TUS9605611A GENERAL INFORMATION:
APPLICANT: Mueller, John P.

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
Mueller, Ellen Elliott
Nye, Steven H.
Pelfrey, Clara M.

APPLICANT

seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-27

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                         US-09-218-277-12 x PCT-US96-05611A-27
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APPLICATION NUMBER: 08/431,644
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 0,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                       620
                                                                                                                                                                       570 CGCCAGCACCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACCGTG 619
                                                                                                                                                                                                                                                          520 GCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGCCAC 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Other nucleic acid DESCRIPTION: PM4 chimera HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05
FILING DATE: 02-MAY-1995
CLASSIFICATION:
                                          52
                                                                                                                               35
                                                                                                                                                                                                  18 rālaSerThrMetAspHisālaArgHisGlyPheLeuProArgHisArgA 35
                                                                                                                                                                                                                                                                                  2 AlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: Double TOPOLOGY: Linear
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                          ACACCGGCATCCTGGACTCCATCGGCCGCTTCTTCGGCGGTGACCGTGGT
GCGCCGAAACGTGGCTCTGGCAAAGTGCCGTGGCTGAAACCGGGCCGTAG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
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T: 1951 Burr Street
Fairfield
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5.259
86.735
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seq_documentation_block:
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                                                                                                                                                                                                                                                            ZIP: 06430

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: MacLintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
                  APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
ADDRESSEE: Maurice N
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 eLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970 TTCGGCTACGGCGGCCGTGCGTCCGACTATAAATCTGCTCACAAAGGCTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 PheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPh 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          870 AAACATTGTGACCCCGCGTACCCCGCCGCCGTCTCAGGGCAAAGGCCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            820 AAATCCCACGGCCGTACCCAGGATGAAAACCCGGTGGTGCACTTCTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Modified Myelin Protein Molecules NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 CCCGCTGCCGTCTCATGCCCGTAGCCAGCCGGGCCTGTGCAACATGTACA 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuProGln 75
                                                                                                                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 02-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Fairfield
STATE: Connecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyArgAspSerArgSerGlySerProMetAlaArgArg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgProGly 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Connecticut
7: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Squinto, Stephen P. Wilkins, James A.
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Mueller, Eileen Elliott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nye, Steven H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lication PC/TUS9605611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maurice M. Klee
                                                                                                                                                                                                                                                    PCT/US96/05611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          919
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 236.00
Ratio: 5.488
Percent Similarity: 100.000
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REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION:
TELEPHONE: (203) 255 1400
TELEPACK: (203) 254 1101
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: PCT-US96-05611A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-218-277-12 x PCT-US96-05611A-8/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application:
                                                                                                                                                                                                                                                                                           APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 4
HYPOTHETICAL: No
ANTI-SENSE: Yes
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 SerHisGlyArgThrGlnAspGluAsnProValValHisPhePheLysAs 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 nIleValThrProArgThrProProProSerGlnGlyLySGlyArgGlyL 110
                                                           COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sir
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Nucleic acid
                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTCCCTGAGCCGTTTCAGCTGGGGCGCC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTGTGACCCCGCGTACCCCGCCGCCGCCGTCTCAGGGCAAAGGCCGTGGCC 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCACGGCCGTACCCAGGATGAAAACCCGGTGGTGCACTTCTTCAAAAA 81
                                                                                                                                                                           06430
                                                                                                                                                                                                                                      Fairfield
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                                                                                                                                                                                                                Connecticut
                                                                                                                                                                                                                                                     1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                             Maurice M. Klee
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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 214.00
Ratio: 5.487
Percent Similarity: 100.000
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEPAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US96-05611A-9
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                   APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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DESCRIPTION: PCR primer oligonucleotide 5
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 yArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyValAspA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 ArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGi 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 laGlnGlyThrLeuSer 152
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FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
                                          COUNTRY: U
ZIP: 06430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic acid
                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: Single
                                                                                                                                          ADDRESSEE: Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAGGGCACCCTGTCC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGTGCGTCCGACTATAAATCTGCTCACAAAGGCTTCAAAGGCGTGGATG
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                                                                                                      Fairfield
                                                           Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                  Application PC/TUS9605611A
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                                                                                                                1951 Burr Street
                                                                                                                                                                                                                                                                                                                                  Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
                                                                                                                                                                                                                                                                                               Matis, Louis A.
Mueller, Eileen Elliott
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Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; HYPOTHETICAL: |
; ANTI-SENSE: NO
PCT-US96-05611A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: PCT-US96-05611A-5 from: 1 to: 130
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                                                                                                                                                                                                                                        Sequence 6, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/431,644
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: MAY 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         _documentation_block:
equence 6, Application PC/TUS9605611A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 1
                      TITLE OF INVENTION: Modified Myelin Protein Molecules NUMBER OF SEQUENCES: 29
                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                                                                              APPLICANT:
                                                                                                  APPLICANT:
                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                              126
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LENGTH: 130 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 255 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                       34 rgAsp 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 ATGGCGTCTCAGAAACGTCCGTCCCAGCGTCACGGCTCCAAATACCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Klee, Maurice M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 0
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                              GTGAC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCGCCAGCACCATGGACCATGCCCGTCATGGCTTCCTGCCGCGTCACC
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                                                                                                                                                    Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                                   Mueller, Elleen Elliott
Nye, Steven H.
                                                                          Pelfrey, Clara M.
Squinto, Stephen P.
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PE: Other nucleic acid
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: 5.371
: 100.000
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                                                           James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US96/05611A
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                          125
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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                  seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-218-277-12 x PCT-US96-05611A-6/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; HYPOTHETICAL: No.; ANTI-SENSE: Yes PCT-US96-05611A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: PCT-US96-05611A-6 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 162.00
Ratio: 5.400
Percent Similarity: 100.000
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APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEPAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     128 CTGCCGCGTCACCGTGACACCGGCATCCTGGACTCCATCGGCCGCTTCTT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 129 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                           46 eGlyGlyAspArgGlyAlaProLysArgGlySerGlyLys 59
                                                                                                                                                                                                                                                                                                                                                                                                            30 LeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPhePh 46
                                                                                                                                                                                                                                                                                                    78 CGGCGGTGACCGTGGTGCGCCGAAACGTGGCTCTGGCAAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US96/05611A FILING DATE: 02-MAY-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Fairfield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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STREET: 1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06430
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DEDNESS: Single
                                                                                                                                                                                            Application PC/TUS9605611A
                                                                               Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1951 Burr Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                       Mueller, Eileen Elliott
Nye, Steven H.
Pelfrey, Clara M.
Squinto, Stephen P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
100.000
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seq_documentation_block:
; Sequence 10, Application PC/TUS9605611A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-218-277-12 x PCT-US96-05611A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                         seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; HYPOTHETICAL: |
; ANTI-SENSE: NO
PCT-US96-05611A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 135.00
Ratio: 5.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: PCT-US96-05611A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (20) .... 7
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE THARACTERISTICS:
133 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear

MOLECULE TYPE: Other nucleic acid

DESCRIPTION: PCR primer oligonucleotide 3

HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: AL TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 255 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   111
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CORRESPONDENCE ADDRESS:
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                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                     59
                                                                                                                                                                                                                    75 nLysSerHisGlyArgThrGln 82
                                                                                                                                                                                                                                                                              61 AAAGACTCCCACCACCCGGCTCGTACCGCGCACTATGGCTCCCTGCCGCA 110
PPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1951 Bu
CITY: Fairfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Klee, Maurice M. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                     LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuProGl 75
                                                                                                                                                                                                 GAAATCCCACGGCCGTACCCAG 132
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            Mueller, John P.
Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurice M. Klee
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) 254 00: 7:
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Gaps: 0
Identity: 100.000
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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-10/rev
                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: Linear nucleic acid; MCIECULE TYPE: Other nucleic acid; DESCRIPTION: PCR primer oligonucleotide 6; HYPOTHETICAL: No; ANTI-SENSE: Yes
PCT-US96-05611A-10
                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                           Quality: 130.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                   Align seg 1/1 to reverse of: PCT-US96-05611A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/ACENT IMPORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REGISTRATION NUMBER: 30,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (203) 255
TELEFAX: (203) 254 11
INFORMATION FOR SEQ ID NO:
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                                                                                            146 AspAlaGlnGlyThrLeuSerLySIlePheLySLeuGlyGlyArgAspSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 111 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
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CORRESPONDENCE ADDRESS:
                                  162 rArgSerGlySerProMetAlaArgArg 171
                                                                          110 GATGCCCAGGGCACCCTGTCCAAAATTTTCAAACTGGGCGGCCGTGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
60
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FILING DATE: 02-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Nucleic acid
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Fairfield
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Squinto, Stephen P.
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Percent Identity: 100.000
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
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Perfect score:
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 60.0 , Gapext 60.0
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171
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           BB
                                             MBCIB
MBCIS
A37246
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12904
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F04117
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hypothetical pro
U24 [imported] -
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myelin basic pro
myelin basic pro
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on	თ	σ	σ	σ	σ	o	σ	σ	σ	თ	თ	7	7	7	7
ω	ω .5	3 .5	ω .5	ω .5	ω	ω	ω .5	ω .5	3 5	ω	ω	4.1	4.1	4.1	4.1
132	125	124	116	116	115	113	109	102	96	88	60	3305	1345	1151	839
N	N	N	N	N	N	N	N	N	N	ν	N	N	N	N	N
T21416	S21419	S49957	S17567	S39434	A23925	S13494	B72213	S61055	G70117	S38267	A57413	T18358	T41960	T18535	T39190
hypothetical prote	hypothetical 14.4K	hypothetical prote	AQN-3 protein - pi			major oleosin chai	conserved hypothet	probable membrane	conserved hypothet	cuticle protein Lm	band 3 anion trans	apolipophorin prec	major capsid prote	high molecular mas	probable ATP-depen

(EC 3. prote (EC 3. prote (EC 3. prote eEC 3.	protein prote prote prote prote	prote prote d] - h	bacte (EC) prote	prote prote	ited,	ds tes/sec
A; Molecule type: protein A; Residues: 2-59,86-197 < PRO> A; Experimental source: brain R; Scoble, H.A.; Whitaker, J.N.; Biemann, F. J. Neurochem. 47, 614-616, 1986 A; Title: Analysis of the primary sequence A; Reference number: A60862; MUID:86280476 A; Accession: A60862	A;Molecule type: protein A;Residues: 2-59,86-197 <ccar> R;Proost, P.; Van Damme, J.; Opdenakker, G. Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993 A;Title: Leukocyte gelatinase B cleavage releases encephalitogens A;Reference number: JH0802; MUID:93282820 A;Accession: JH0802</ccar>	Biochem. J. 123, 57-67, 1971 A; Title: Amino acid sequence of the encephalitogenic A; Reference number: A90256; MUID:72066400 A; Accession: A90256	A; Molecule type: mRNA A; Residues: 1-197 (RAZ) A; Note: antibody to the exon 2 encoded sequence A; Note: a 17.2% splice form is also described A; Note: antibody to the exon 2 encoded sequence R; Carnegie, P.R.	A; Molecule type: mRNA A; Residues: 1-59, 86-197 < KAM> A; Cross-references: GB:M13577; NID:g187408; A; Note: 18.5K splice form A; Accession: B94106	MEBULT 1 MEBUB MEHUB myelin basic protein - human N;Contains; myelin basic protein precursor, 17.2K splice form; myelin basic; SK splice form C;Species; Homo sapiens (man) C;Date: 18-Dec-1981 *sequence_revision 25-Aug-1995 *text_change 22-Jun-1999 C;Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; R;Streicher, R; Stoffel, W Biol. Chem. Hoppe-Seyler 370, 503-510, 1989 A;Title: The organization of the human myelin basic protein gene. Comparison A; Reference number: S10482; MUID:89302693 A;Accession: S10482 A;Status: translation not shown A;Mesidues: 1-197 <str> A;Cross references: EMBL:X17286; NID:g34490; PIDN:CAA35179.1; PID:e221974; P Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986 A;Title: Identification of three forms of human myelin basic protein by cDNA A;Reference number: A94106; MUID:86259714 A;Accession: A94106</str>	30 7 4.1 839 2 T39190 31 7 4.1 1151 2 T18535 32 7 4.1 1345 2 T18536 33 7 4.1 3305 2 T18358 34 6 3.5 60 2 A57413 35 6 3.5 96 2 G70117 37 6 3.5 102 2 S61055 38 6 3.5 113 2 S172213 39 6 3.5 113 2 S172213 39 6 3.5 115 2 A23925 41 6 3.5 116 2 S39434 42 6 3.5 116 2 S39434 43 6 3.5 116 2 S39434 44 6 3.5 124 2 S49957 44 6 3.5 125 2 S21419 45 6 3.5 132 2 T21416
K. of human myelin basic protein peptides 1-44	G. 1181, 1993 releases encephalitogens from human myelin b	halitogenic basic protein from human ${}_{ackslash}$ myelin.	squence detected a 21.5K splice form :bed squence detected a 21.5K splice form; a 17.2K)8; PIDN:AAA59562.1; PID:g307160	Por, 17.2K splice form; myelin basic protein gene. Comparison with the principle protein gene. Comparison with the protein pro	probable ATP-depen high molecular mas major capsid prote apolipophorin prec band 3 anion trans cuticle protein Lm conserved hypothet probable membrane conserved hypothet major oleosin chai proline-rich phosp spermadhesin AQN-3 AQN-3 protein - pi hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

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A;Molecule type: protein
A;Residues: 2-45;117-197 <SCO>
A;Residues: 2-45;117-197 <ACC
A;Attle: Amino acid sequence of human myslin basic protein peptide 45-89 as determined because the protein and acid sequence of human myslin basic protein peptide 45-89 as determined because type: protein
A;Reference number: A61420; MUID:84185608
A;Reference number: A59,86-116 <AGIB>
R;Wood, D.D.; Moscarello, M.A.
J. Biol. Chem. 254, 5121-5127, 1989
A;Reference number: A33273; MUID:89174797
A;Reference number: A33273; MUID:89174797
A;Reference number: A33273; MUID:89174797
A;Reference number: A33273; MUID:89174797
A;Residues: 15-25; X', 27-31, 'X', 33-59,86-148,'X', 150-156,'X', 158-185,'X', 187-196,'X' <ACC
A;Note: form C-8; residues designated 'X' were determined as citrulline
A;Molecule type: protein
A;Reference number: A9205; MUID:72066401
A;Contents: annotation; methylarginine
A;Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx
B;Contents: annotation
A;Note: A readon including residues 139-149 indices experimental antoimume encephalanced
A;Note: A readon including residues 139-149 indices experimental antoimume encephalanced
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A; Title: Repetitive DNA (TGGA)n 5' to the human myelin bas A; Reference number: I54219; MUID:90152679

A; Accession: I54219

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-59 CARSS>

A; Cross-references: GB:M63599; NID:9187402; PIDN:AAA59560.

R; Roth, H.J.; Kronquist, K.E.; Kerlero de Rosbo, N.; Crand J. Neurosci. Res. 17, 321-328, 1987

A; Title: Evidence for the expression of four myelin basic A; Reference number: I56567; MUID:87311781

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Status: preliminary; translated from GB/EMBL/DDBJ
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Residues: 1-132,144-197 <RE2>
Cross-references: GB:M30516; NID:g187410; PIDN:AAA59563.1; PID:g307161
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A;Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
C;Function:
A;Description: probably helps maintain myelin structure
C;Superfamily: myelin basic protein
C;Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto
C;CKeywords: acetylated amino end; alternative splice form #status predicted <MATI>
F;2-197/Product: myelin basic protein, 21.5K splice form #status predicted <MF;2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <F;2-59,86-197/Product: myelin basic protein, 18.5K splice form #status experimental <F;2-59,86-132,144-197/Product: myelin basic protein, 17.2K splice form #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,149,157,180,197/Modified site: citrulline (Arg) (in form C-8) #status experimental F;26,32,449,457/Mo
                      myelin basic protein S - rat
N;Alternate names: small myelin basic protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change
C;Accession: B24351; A90275; A94243; A21062; A03142
R;Schalch, M.; Budzinski, R.M.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
A;Title: Cloned proteolipid protein and myelin basic protein cDN
A;Reference number: A24351; MUID:87026249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-171 <WES>
C; Comment: This protein may function in maintaining the proper structure of myelin.
C; Comment: This protein may function in maintaining the proper structure of myelin.
C; Superfamily: myelin basic protein
C; Keywords: blocked amino end; methylated amino acid; myelin; structural protein
F; 1, Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F; 107/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg
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R;Westall, F.C.; Thompson, M.; Kalter, S.S.
Life Sci. 17, 219-223, 1975
A;Title: The proposed sequence of the encephalitogenic A;Reference number: A03139; MUID:76009821
A;Accession: A03139
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1987 *sequence_revision
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A; Accession: B24351
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Matches 113; Conserv
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Pred. No. 2.3e-112;
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2 ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFG

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A; Accession: Aziv...
A; Accession: Aziv...
A; Molecule type: mRNA
A
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A:Residues: 46-86 <MCF>
A:Residues: 46-86 <MCF>
A:Residues: Ho-sequence reported for this encephalitogenic peptide differs
R:Roach, A.; Boylan, K.; Horvath, S.; prusiner, S.B.; Hood, L.E.
Cell 34, 799-806, 1983
A:Title: Characterization of cloned cDNA representing rat myelin basic
A:Reference number: A21062; MUID:84026484
A:Accession: A21062
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Biochem. J. 141, 243-255, 1974
A;Title: Amino acid sequence of the smaller
A;Reference number: A90275; MUID:75127359
A;Accession: A90275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change
C;Accession: A37246; C92087; A03140
R;Deibler, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.
J. Neurochem. 43, 100-105, 1984
A;Title: Sequence of guinea pig myelin basic protein.
A;Reference number: A37246; MUID:84215086
A;Accession: A37246
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A;Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen: A;Reference number: A94243; MUID:73180720
                                                                                                                                                                                                                                                                                                         R;Shapira, R.; McKneally, S.S.; Cho
J. Biol. Chem. 246, 4630-4640, 1971
A;Title: Encephalitogenic fragment
A;Reference number: A92087
A;Accession: C92087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-167 <DEI>
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A; Residues: 1-128 <SCH>
A; Cross-references: EMBL:M25889; NID:g205321;
                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 45-87 <SHA>
   Query Ma
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Matches
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Residues: 2-128
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                            Score 46;
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-191, 'SSEP' < CAM2>
A; Residues: 1-191, 'SSEP' < CAM2>
A; Cross-references: GB:L07508; NID:g193586; PIDN:
A; Experimental source: clone BG21
A; Note: sequence extracted from NCBI backbone (NC
R; de Ferra, F:; Engh, H:; Hudson, L:; Kamholz, J.
Cell 43, 721-727, 1985
A; Title: Alternative splicing accounts for the fo
A; Reference number: A90875; MUID:86079555
A; Accession: A90875;
                                                                                      A:Accessum. A:Accessum. A:Accessum. A:Rolecule type: mRNA
A:Rolecule type: mRNA
A:Residues: 134-190;217-263;275-328 <NEW2>
A:Residues: 134-190;217-263;275-328 <NEW2>
A:Cross-references: GB:M15062; NID:g199050
A:Experimental source: clone M78; splice form 17
R:Kitamura, K.; Newman, S.L.; Campagnoni, C.W.; '
J. Neurochem. 54, 2032-2041, 1990
A:Title: Expression of a novel transcript of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 134-328 <DEF>
A;Cross-references: GB:L00404; GB:M11669; NID:g199060; PIDN:AAA39502.1;
A;Experimental source: 21.5K
R;Takahashi, N; Roach, A; Teplow, D.B.; Prusiner, S.B.; Hood, L.
Cell 42, 139-148, 1985
A;Title: Cloning and characterization of the myelin basic protein gene f
A;Reference number: A90867; MUID:85254913
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N;Alternate names: golli-mbp protein; MBP
N;Contains: myelin basic protein
N;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
C;Accession: A45421; B45421; A90875; A90867; A26591; B26591; A60920; I48407; C;Accession: A45421; B45421; A90875; A90867; A26591; B26591; A00920; I48407; R;Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kampf, K.; Anur-Umarjee, J. Biol. Chem. 268, 4930-4938, 1993
J. Biol. Chem. 268, 4930-4938, 1993
A;Title: Structure and developmental regulation of Golli-mbp, a 105-Kilobase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 134-190;217-328 <TAK>
A;Residues: 134-190;217-328 <TAK>
A;Cross references: GB:M11533; NID:g199044; PIDN:AAA39496.1;
A;Experimental source: 18.5K
R;Newman, S.; Kitamura, K.; Campagnoni, A.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
A;Title: Identification of a CDNA coding for a fifth form of
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A;Accession: A45421
A;Molecule type: mRNA
A;Residues: 1-190;217-276;316-328 <CAM1>
A;Cross references: GB:L07507; NID:g193584
A;Experimental source: clone J37
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A; Molecule type: mRNA
A; Residues: 134-190; 217-274; 316-328
                                                          A; Status: translation not shown
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A;Accession: A26591
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14K

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C;Function:
A;Description: probably helps maintain myelin structure
C;Superfamily: myelin basic protein
C;Superfamily: myelin basic protein
C;Reywords: alternative splicing; myelin; structural protein
C;Reywords: alternative splicing; myelin; structural protein
C;Reywords: alternative splicing; myelin; structural protein
F;1-190, 217-276, 316-328/Product: Goll: mbp protein (clone J37) #status predicted <MAT>
F;134-328/Product: myelin basic protein, splice form 17K-a #status predicted <MAT
F;134-190, 217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MAT
F;134-190, 217-263, 275-328/Product: myelin basic protein, splice form 17K-b #status predict
F;134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predict
F;134-190, 217-274, 316-328/Product: myelin basic protein, splice form 14K #status predict
myelin basic protein - bovine
M;Alternate names: myelin Al protein
N;Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 07-May-1999
C;Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
R;Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
J. Biol. Chem. 246, 5770-5784, 1971
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A;Title: The promoter elements of the mouse myelin basic prot A;Reference number: I54033; MUID:89252919
A;Accession: I54033
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-191, 'SSEP' <GRI>
A;Residues: 1-191, 'SSEP' <GRI>
A;Cross-references: EMBL:X67319; NID:g51332; PIDN:CAA47733.1; PID:g51333
A;Note: submitted to the EMBL Data Library, July 1992
R;Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
A;Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin A;Reference number: I58996; MUID:84119431
A;Accession: I58996
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A;Molecule type: DNA
A;Residues: 217-229, 'HN', 232-250 <OKA>
A;Residues: 217-229, 'HN', 232-250 <OKA>
A;Cross-references: GB:M36275; NID:g199069; PIDN:AAA39504.1; PID:g293725
A;Note: hypothetical translation of the reversed and complementary sequence to C;Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.24K,
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A;Residues: 134-157 <MIU>
A;Residues: 134-157 <MIU>
A;Cross-references: GB:M24410; NID:g199052;
R;Okano, H; Tamura, T; Miura, M; Aoyama,
EMBO J. 7, 77-83, 1988
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A; Introns: 190/3; 250/3; 2
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A;Accession: I53256
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A;Residues: 219-248 <ZEL>
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A; Accession: I48407
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Best Local Similarity
Matches 45; Conserv
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. 59, 2318-2323,
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23, 1992
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Pred. No.
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7e-40;
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Oshimura, M.;
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17.22K an
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   myelin basic protein - N; Alternate names: mye
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1.'S', 2-169 <EYL>
R; Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, J
J. Blol. Chem. 249, 559-567, 1974
A; Title: Specific cleavage of the Al protein from
                                                                                                                                                                                                                                    A;Note: the region including residues 114-122 induces experimental allergic encephalo () Superfamily: myelin basic protein c;Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune ence F;1-169/Product: myelin basic protein #status experimental <AMT> F;1-16/Product: myelin peptide amide-16 #status experimental <PA16> F;1-17/Product: myelin peptide amide-12 #status experimental <PA12> F;1-17/Product: myelin peptide amide-12 #status experimental <PA12> F;1-17/Product: myelin peptide amide-0 end (Ala) #status experimental = F;12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide F;16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide F;16/Modified site: omega-N-methylarginine or omega-N-omega-N-dimethylarginine (Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hid
Blochem. J. 306, 551-555, 1995
A;Tille: S100-beta is a target protein of
A;Reference number: S54343; MUID:95194333
A;Accession: S54343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Contents: annotation
A;Contents: annotation
A;Note: Arg-106 is modified to monomethylarginine and dimethylarginine
R;Eylar, E.H.; Caccam, J.; Jackson, J.J.; Westall, F.C.; Robinson, A.B.
Science 168, 1220-1223, 1970
A;Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing
A;Reference number: A94241; MUID:70178977
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A; Residues: 1-16 <TA2>
A; Residues: 1-16 <TA2>
A; Rote: these peptides have carboxyl-terminal amides probably produced
R; Brostoff, S.; Eylar, E.H.
Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
A; Title: Localization of methylated arginine in the Al protein from mye
A; Reference number: A93777; MUID:71153946
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A; Accession: A61641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 74-75, 'HG', 78-82, 'D', 84-88; 105, 'X', 107-108, 'X', 110-114, 'X', 116-119
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A; Reference number:
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QDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAEGQ
                                                                                                           l Similarity
41; Conser
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llarity 100.0%;
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Pred. No. 7.2
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-14 <TAK>
A; Residues: 1-14 <TAK>
A; Note: the sequence in the abstract is inconsistent with that in figure 3 in having Gl
A; Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic
C; Superfamily: myelin basic protein
C; Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enceph
F; 1-171/Product: myelin basic protein #status experimental <AMI>
F; 1-14/Product: myelin peptide amide-14 #status experimental <PAI2>
F; 1-74/Product: myelin peptide amide-14 #status experimental
F; 14/Modified site: acetylated amino end (Ala) #status experimental
F; 14/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide am
F; 14/Modified site: omega-N-methylarginine or omega-N, omega-N'-dimethylarginine (Arg)
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Apr:1996 #sequence_revision 26-Apr-1996 #text_change 07-May-1999
C;Accession: A61640; A36245
R;Kita, J.; Deibler, G.E.; Krutzsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A;Title: Amino acid sequence of porcine myelin basic protein.
A;Reference number: A61640; MUID:85056964
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Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
A:Reference number: A36245; MUID:91058553
A:Accession: A36245
myelin basic protein - rabbit (fragment)

N;Alternate names: myelin Al protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1991 **sequence_revision 30-Sep-1991 **text_change
C;Accession: B92087; A03140
R;Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RISANGHERA, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L. FEBS Lett. 273, 223-226, 1990
A;Title: Identification of the sites in myelin basic protein that are phosphorylated A;Reference number: S12904; MUID:91032186
A;Accession: S12904
A;Accession: S12904
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A;Molecule type: protein
A;Residues: 1-14 <SAN>
C;Keywords: phosphotransi
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C:Date: 19-Mar-1997 #sequence_revision
C:Accession: S12904
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Matches
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Pred. No.
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. 4.5e-08;
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hypothetical

protein

U24 [imported]

human herpesvirus

(strain

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J. Biol. Chem. 246, 4630-4640
A;Title: Encephalitogenic fra
A;Reference number: A92087
A;Accession: B92087
A;Molecule type: protein
A;Residues: 1-42 <SHA>
C;Superfamily: myelin basic p.
C;Keywords: myelin
                                                                                                                                                                                                                                                                                                RESULT 11
A60222
A60222
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 17-Jul-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S08535
R;Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A;Title: Developmental accumulation and heterogeneity of myelin basic protein transcr A;Reference number: S08535; MUID:89358239
A;Accession: S08535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myelin basic protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-174 <ZOP>
A; Cross-references: EMBL: X17103; NID: g63594; PIDN: CAA34959.1; PID: g63595
C; Superfamily: myelin basic protein
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                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-33 <ARU;
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F;Aruga, J.; Okano, H.; Mikoshiba, K.
J. Neurochem. 56, 1222-1226, 1991
A;Title: Identification of the new isoforms of mouse myelin basic protein: the existe A;Reference number: A60222; MUID:91162193
A;Accession: A60222
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23
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GRGLSLSRFSW 33
                                                                                 Similarity
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100.0%; Pred. No.
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J. Virol. 68, 597-610, 1994
A.Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of A;Reference number: Z16644; MUID:94118404
A;Recession: T09318
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-93 CNIC>
A;Cross-references: EMBL:L25528; NID:g451932; PID:g451949
C;Genetics:
                                                                                                                                                                                                                                   EOLF1 protein - human herpesvirus 6 (strain UllU2)
C;Species: human herpesvirus 6
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09318
R;Nicholas, J; Martin, M.
J. Virol. 68, 597-610. 1904
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A;Variety: strain HST
G:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43984
R;Isegawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa J. Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: Z22732
A;Accession: T43984
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C;Specles: human herpesvirus 6
A;Varlety: strain Z29
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T44170
R;Dominguez, G; Dambaugh, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. virol. 73, 8040-8052, 1999
A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human A;Title: Human herpesvirus 6B genome sequence: coding content and comparison with human A;Reference number: Z22734; MUID:99412318
A;Accession: T44170
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-88 < DOM>
A;Cross-references: EMBL:AF157706;
A;Experimental source: strain Z29;
C;GenetLcs:
A;Note: U24
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100.0%; Pred. No. 5.9;
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Search completed: September 26, 2000, 19:37:20 Job time: 166 sec

A; Gene: EoLF1

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C;Accession: A69884

R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.N.; Alloni, G, Azevedo, V.; Ber R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Fezrari, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Fezrari, A.; Aluthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A; Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstta, P.; Tognanoi, A.; Tosato, V.; Uchlya A; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-123 <KUN>
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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71 RPGFGYG 77
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ce: strain 168
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MBP_PANTR
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MBP_RAT
MBP_BOVINE
MBP_BOVINE
MBP_BOVINE
MBP_PIG
MBP_CHICK
MBP_CAVP
MBP_CAV
 PHNN_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P02686 homo sapien
P06906 pan troglod
P25188 cavia porce
P02688 rattus norv
                                                                                                                                                                                                                                                             P15720
Q91325
Q91325
P801483
P20939
P533295
P533295
P538919
P43007
P54280
                     Q25490
P801232
P801238
Q60885
P24020
P40542
P35086
P35086
P306604
P771662
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                                                                                                              0 mus musculu
1 bus taurus
8 sus scrofa
4 oryctolagus
9 allus gall
5 raja erinac
9 squalus aca
3 amphidinium
9 heterodontu
5 saccharomyc
7 rattus norv
9 equine herp
1 homo sapien
0 caenorhabdi
1 herpes simp
0 randuca sex
2 locusta mig
8 stylonychia
5 mus musculu
1 sus scrofa
2 saccharomyc
6 synechococc
6 synechococc
6 synechococc
6 synechococc
6 synechococc
O pseudorabie
2 escherichia
9 zea mays (m
4 oryza sativ
5 oryctolagus
0 escherichia
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Result No.

45	44	43	42	41	40	.	38	37	36	35	34	
σ	σ	o	a	o	o	o	σ	σ	σ	o	σ	
3.5	ω .5	ω .5	3 5	ω .5	ω	ω .5	ω	ω	ω .5	ω	ω 	
253	251	251	249	249	244	225	217	214	206	186	186	
بر	J3	μ	μ	μ	Н	\vdash	μ	Ь	Н	Н	H	
CHIQ_TOBAC	YAT8_SCHPO	TPIS_COPCI	YDD1_SCHPO	YBFT_BACSU	FNRA_PSEST	Y638_METJA	UNG_PSEDE	DCOP_THEAC	Alai_MOUSE	TRIS_RAT	TRIS_HUMAN	
P17514 nicotiana t	Q10153 schizosacch	Q12574 coprinus ci	Q10426 schizosacch	O31458 bacillus su	P47200 pseudomonas	Q58055 methanococc	P29950 pseudomonas	074110 thermoplasm	Q63805 mus musculu	P13413 rattus norv	P19237 homo sapien	•

ALIGNMENTS

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SEQUENCE OF 45-58 AND 85-114, AND REVISIONS. Shapira R., McKneally S.S., Chou F., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovine, rabbit, guinea pig, monkey, and human fragments."; J. Biol. Chem. 246:4630-4640(1971).	SEQUENCE OF 1-58 AND 85-196. MEDLINE; 72066400. Carnegie p.R.; "Amino acid sequence of the encephalitogenic basic protein from human myelin."; Biochem. J. 123:57-67(1971).	SEQUENCE OF 1-58 AND 85-196 FROM N.A. MEDLINE; 86259714. Kamholz J., de Ferra F., Puckett C., Lazzarini R.A.; "Identification of three forms of human myelin basic protein by cDNA cloning."; proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).	SEQUENCE OF 1-58; 85-131 AND 143-196 FROM N.A. MEDLINE; 86308101. Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F., Campagnoni A.T.; "Isolation and characterization of a cDNA coding for a novel human 17.3K myelin basic protein (MBP) variant."; J. Neurosci. Res. 16:227-238(1986).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 87311781. Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F., Campagnoni A.T.; "Evidence for the expression of four myelin basic protein variants in the developing human spinal cord through cDNA cloning."; J. Neurosci. Res. 17:321-328(1987).	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE; 89302693. Streicher R., Stoffel W.; "The organization of the human myelin basic protein gene. Comparison with the mouse gene."; with the mouse gene."; Biol. Chem. Hoppe-Seyler 370:503-510(1989).	MBP_HUMAN STANDARD; PRT; 196 AA. P02686; P02686; P1. Ol. Created) Ol.NOV-1991 (Rel. 01, Created) 15-FEB-2000 (Rel. 39, Last annotation update) MYELIN BASIC PROTEIN (MBP). MBP. HOMO sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	TLT 1

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144 AEGQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR

196

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Query Match
Best Local Similarity
Matches 113; Conserv
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EMBL: M30515; AAA5956

EMBL: M30515; AAA5955

EMBL: M30047; AAA5955

EMBL: X17286; CAA3517;

EMBL: X17287; CAA3517;

EMBL: X17290; CAA3517;

EMBL: X17298; CAA3517;

EMBL: X17288; CAA3517;

EMBL: X17289; CAA3517;

EMBL: X16482; S10482.

MIM; 159430; -.
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SEQUENCE
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PRINTS; PR00212; MYELINMBP.
PROSITE; PS00569; MYELIN_MBP;
Myelin; Structural protein; Ac
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"Isolation and partial characterization of methylated the encephalitogenic basic protein of myelin.";
Biochem. J. 123:69-74(1971).
-I- EUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROTEIN MAY FUNCTION FUNCTION FUNCTION TO MAINTAIN PROTEIN PROT
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MEDLINE; 90152679.
Boylan K.B., Ayres T.M.,
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new form of oligonucleotide
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AEGGRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR 171
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ructural protein; Acetylation; Methylation;
encephalomyelitis; Alternative splicing.
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INDUCES EXPERIMENTAL AUTOIMMUNE
ENCEPHALOMYELITIS IN MONKEYS, RABBITS,
AND RATS BUT NOT IN GUINEA PIGS.
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RESULT 2

MBP_DANTR

ID MSP_PANTR

AC P06906;

DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 0
DT 01-JAN-1988 (Rel. 3

DE MYELIN BASIC PROTEI
GN MSP.

OS Pan troglodytes (Ch
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria;
RN [1]

RP PRELIMINARY SEQUENC
RX MEDLINE; 76009821.

RA Westall F.C., Thomp
RT The proposed seque
RT Chimpanzee brain.";
RL Life Sci. 17:219-22
CC -1- FUNCTION: THIS
CC OF MYELIN
CC -1- SUBCELLULLAR LOC
CC -1- SUBCELLOR RUB
RT MEDAR RUB
RT MEDA
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Best Local
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Life Sci. 17:219-223(1975).
-I- FUNCTION: THIS PROTEIN MORE THE PROTEIN MORE THE PROTECTION: CY-1- SUBCELLULAR LOCATION: CY-1- SIMILARITY: BELONGS TO I
                                                                                                                                  SEQUENCE.
MEDLINE; 842150
Deibler G.E., 1
"Sequence of go
                                                                                                                                                                                                                                                                                            MBP_CAVPO STANDARD; PRT; 1
P25188;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-FEB-2000 (Rel. 39, Last annotation
MYELIN BASIC PROTEIN (MBP).
SEQUENCE OF 45-87.
Shapira R., McKneally S.S., Chou F., Kibler R.F.;
"Encephalitogenic fragment of myelin basic protein.
sequence of bovine, rabbit, guinea pig, monkey, and
                                                                                                                                                                                                                                         Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Westall F.C., Thompson
"The proposed sequence
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Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0212; MYELINMBP.
PROSITE; PS00569; MYELIN_MBP; 1.
Myelin; Structural protein; Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE.
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                                                                                                                . Neurochem.
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l similarity 100.0%;
76; Conservative
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171 AA;
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(Rel. 39, Last a
C PROTEIN (MBP).
                                                                                                              ., Martenson R f guinea pig m m. 43:100-105(
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myelin
5(1984)
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METHYLATION (BY SIMILARITY).
; E9FED59DE6933293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76;
Pred. No.
                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Hystricognathi; Cavidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
                                                                                                                                                     Krutzsch
                                                                                                                                    basic
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protein.
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1.8e-72;
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Amino acid human fragments.";
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Best Local S
Matches 46
                                                                                                                                                                                                                SEQUENCE;
                                                                                                                                                                                                                                                                                                                     MEDLINE; 75127359.

Dunkley P.R., Carnegie I
"Amino acid sequence of
myelin.";
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P02688;
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PIR;
                                                                              "Experimental allergic encephalomyelitis encephalitogenic proteins and peptides.", science 179:478-480(1973).

-i- FUNCTION: THIS PROTEIN MAY FUNCTION 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYELIN
MBP.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-FEB-2000 (Rel.
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SUBCELLULAR LOCATION: CY

SIMILARITY: BELONGS TO THE STATE OF S
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- FUNCTION: THIS PROTEIN MAY FUNCTION
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          SUBCELLULAR
ALTERNATIVE
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llarity 100.0%;
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01, Last sequence up
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ein and myelin basic protein
genes during myelination.";
367:825-834(1986).
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     CYTOPLASMIC S:
RATS HAVE TWO
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[3]
SEQUENCE FROM
MEDLINE; 87118269.
A Newman S., Kitamura K., C
T "Identification of a cDN"
--tein in mouse.";
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EMBL; K00512; -; NOT_ANNOTAT
PIR; A03142; MARRYS.
PIR; B24351; B24351.
PIR; B24351; B24351.
PIR; A21062; A21062; A21062;
PFAM; PFO1669; Myelin_MBP; 1
PRINTS; PRO0212; MYELINMBP.
                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1987
01-JAN-1988
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                           MBP_MOUSE P04370;
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                                                                                                                          Takahashi N., Roach A., Teplow D.B., I "Cloning and characterization of the r mouse: one gene can encode both 14 kd use of exons.";
                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                               'Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMALLER ONE, SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESIDUE 113 OR 114) WITH RESPECT TO THE LARGER ONES FROM OTHER SPECIES. SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
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                                                                                                          42:139-148(1985).
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l Similarity 100.
45; Conservative
                                                                                                                                                                        FROM N.A.
85254913.
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86079555.
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encephalomyelitis; Alternative
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C PROTEIN (
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METHYLATION (MONO-:44% C

SG -> GS (IN REF. 4).

M -> I (IN REF. 2).

M -> B4C9F33C19A9E137 CRC64
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Pred. No. 5.1
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Sciurognathi;
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kd and 18.5 kd MB
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thi; Muridae;
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Autoimmune
INIT_MET
MOD_RES
MOD_RES
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"The promoter elements of the mouse myelin basic protein getion efficiently in NG108-15 neuronal/glial cells.";
Gene 75:31-38(1989).
-I- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER
OF MYELIN.
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MEDLINE; 89252919.
Miura M., Tamura 1
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ALTERNATIVE
KDA, 17 KDA
                M; PF01669; Myelin_MBP; 1.

NITS; PR00212; MYELINMBP; 1.

SITE; PS00569; MYELIN_MBP; 1.

Liin; Structural protein; Acetylation; Metroimmune encephalomyelitis; Alternative sprommune encephalomyelitis; A
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M11539 AAA39496.11
M11530 AAA39496.11
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A26591; A26591.
B26591; B26591.
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18.5 kDa ISOFORM
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MBP_BOVIN

MBP_BOVIN

AC P02687;

AC P02687;

DT 21_JUL-1986 (Rel. 01, Created)

DT 21_JUL-1986 (Rel. 01, Last sequence update)

DT 21_JUL-1986 (Rel. 01, Last sequence verteb)

GN MBP.

OC Bukaryota; Metazoa; Chordata; Craniata; Verteb)

GN MBP.

OC Bukaryota; Metazoa; Chordata; Craniata; Verteb)

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NEDLINE; OF SOVINGE; Bos.

RX MEDLINE; T2007306.

RX MEDLINE; T2007306.

RX MEDLINE; T2007306.

RX MEDLINE; T2007306.

RX MEDLINE; T4070688.

RX Shapira R., McKneally S.S., Chou F., Kibler R.

RI "Scephalitogenic fragment of myelin basic pro

J Biol. Chem. 246:4530-4640(1971).

RX MEDLINE; T0178977.

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Best Local S
Matches 45
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Brostoff S.W., Eylar E.H.;
"Localization of methylated arginine in the Al protein Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shapira R., McKneally S.S., Chou F., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein. sequence of bovine, rabbit, guinea pig, monkey, and J. Biol. Chem. 246:4630-4640(1971).
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                                                                                                                                                                                                                                                                                                                                                 Sylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson Experimental allergic encephalomyelitis: synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
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45; Conserv
ve encephalomyelitis.
1 1 1 A.
106 106 ME
114 122
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45;
Pred. No.
                      ACETYLATION.
METHYLATION (MONO- OR DI-).
INDUCES EXPERIMENTAL AUTOIMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORM).
MISSING (IN 17 kDa ISOFOR ISOFORM).
D208CACOCF52ACD2 CRC64;
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                                                                                                             Methylation;
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                                                                                                                                                                                                                                                                                     MAINTAIN PROPER
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human
                                                                                                           Phosphorylation;
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fragments.
                                                                                                                                                                                                                                                                                     STRUCTURE
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OF MYELIN. C PROTEIN FAMILY.

STRUCTURE

2e-06;

0 Length

Indels

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Gaps

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CRC64

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RESULT
MBP_RAI
ID MBP_RAI
ID P
AC P
DT 0
DT 0
DT 0
DT 0
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CO C
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MBP_PIG
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 41
                                                                                                                                                           MBP_RABIT
P25274;
01-MAY-1992 (
01-MAY-1992 (
15-FEB-2000 (
MYELIN BASIC
                                                                                                                                                                                                                                                                      RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 85056964.

Ira J.-I., Deibler G.E., Krutzsch H.C., Martenson R.E.;

"Amino acid sequence of porcine myelin basic protein.";

J. Neurochem. 44:134-142(1985).

-!- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBP_PIG
P81558;
                                                                            MYELLA ..... MYELLA E.M. (Rabbit).
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
MYELIN BASIC PROTEIN (MBP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
   Shapira R., McKneal "Encephalitogenic f sequence of bovine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF MYELIN.
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                                                                                                                                                                                                                                                                                                                                                                                                         h 24.0%; S
Similarity 100.0%;
41; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PS00569; MYELIN_MBP;
Structural protein; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 AA;
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                                                                                                                                                  (Rel. 22, Created)
(Rel. 22, Last sequence update)
(Rel. 39, Last annotation updat
C PROTEIN (MBP) (MYELIN A1 PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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llarity 100.0%;
Conservative
                                       McKneally
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                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BELONGS TO
ally S.S., Chou F., Kibler R.F.; fragment of myelin basic protein. e, rabbit, guinea pig, monkey, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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METHYLATION (MONO- OR DI-) (DA SIMILARITY).

SIMILARITY).

INDUCES EXPERIMENTAL AUTOIMMUNE ENCEPHALOMYELITIS (BY SIMILARITY)

~~7AFDF2F24028D9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE MYELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acetylation; Methylation; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB; Pred. No. 1.1
0; Mismatches
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Pred. No. 1e-
0; Mismatches
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8E1157B7A1978484
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                                                                                                                                                          update)
PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                   42
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. 1.1e-35;
                                                                                     Vertebrata; Euteleostomi; ae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
le-35;
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C PROTEIN FAMILY
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     Amino
human
   acid
fragments.";
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                                                  Query Match
Best Local S
Matches 12
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Best Local
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P15720;
01-APR-1990
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NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zopf D., Sonntag H., Betz H., Gundelfinger E.I
"Developmental accumulation and heterogeneity
transcripts in the chick visual system.";
Glia 2:241-249(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR 1990 (Rel. 14, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
MYELIN BASIC PROTEIN (MBP).

Gallus gallus (Chicken).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>+</del> <del>+</del> <del>+</del>
                                                                                                                                        PRINTS; PR00212; MYELINMBP.

PROSITE; PS00569; MYELLN_MBP; 1.

                                                                                                                                                                                                                           EMBL; X17103; CAA34959.1; --
PIR; S08535; S08535.
PFAM; PF01669; MYELIN_MBP; 1.
PRINTS; PR00212; MYELIN_MBP.
PROSITE; PS00569; MYELIN_MBP;
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-WHITE LEGHORN;
MEDLINE; 89358239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; B92087; B92087.
PROSITE; PS00569; MYELIN_MBP;
                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                   148 QGTLSKIFKLGG
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- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DRGAPKRGSGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF MYELIN.
SUBCELLULAR LOCATION: CYTOPLASMIC
SIMILARITY: BELONGS TO THE MYELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF MYELIN.
                                                  Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein;
                                                                                                                                      105
173 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42
                                                  7.0%; S llarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN MAY FUNCTION TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BRAIN
                                                  Score 12; DB Pred. No. 3.1 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P; PARTIAL.
Autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12;
Pred. No.
                                                                                                                                      ACETYLATION (BY SIMILARITY).
METHYLATION (BY SIMILARITY).
HABFE70D4C9CF019D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E283198F53F6DE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIDE C
                                               DB 1;
3.1e-05;
0;
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MAINTAIN

PROPER

STRUCTURE

.ch/announce/

Length 173;

0

Gaps

0

у of

myelin

basic

protein

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146 QGTLSKIFKLGG

157

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RESULT 11

MBP_SCC
ID MBP_SC
AC Q91433
DT 01-NOV
DT 01-NOV
DT 15-FEE
DE MYELIN
GN MBP
OC Eukar)
OC Elasmc
RN [1]
RP SEQUEL
RC TISSUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
                                                                                              MBP_SQUAC
Q91439;
Q1-NOV-1997
Q1-NOV-1997
15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MBP_RAJER
Q91325;
01-NOV-1997
01-NOV-1997
SEQUENCE FROM
TISSUE-BRAIN,
                                                                                                                                                                                                                                                                                                 INIT_MET
MOD_RES
VARIANT
VARIANT
SEQUENCE
                                         Squalus acanthias (Spiny dogfish)
Eukaryota; Metazoa; Chordata; Cra
Elasmobranchii; Neoselachii; Squa
                                                                                                                                                                                                                                                                                                                                                                   PRINTS; I
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular cloning of the myelin k acanthias, and the ray, Raja erina J. Neurosci. Res. 35:577-584(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Elasmobranchii, Neoselachii; Squalea; Hypnosqualea;
Batoidea; Rajiformes; Rajidae; Rajinae; Raja.
                               Elasmobranchii;
[1]
                                                                                     MYELIN
                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spivack W.D., Zhong N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2000
MYELIN BASIC
                                                                                                                                                                                                  73
                                                                                                                                                                                                            86 PVVHFFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
                                                                                                                                                                                                  PVVHFFKN
                                                                                                                                                                                                                                                                                                                                                                                      U44053; AAA96756.1; -. PF01669; Myelin_MBP; 1.
                                                                                     BASIC
                                                                                                                                                                                                                                            h 4.7%;
Similarity 100.0%
8; Conservative
                                                                                                                                                                                                                                                                                                                                                         Structural
                                                                                                                                                                                                                                                                                                                                                                   PR00212; MYELINMBP. PS00569; MYELIN_MBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAIN, AND SPINAL CORD;
94016687.
                                                                                   7 (Rel. 35, Created)
7 (Rel. 35, Last seque)
0 (Rel. 39, Last anno:
IC PROTEIN (MBP).
                                                                                                                                                                                                                                                                                                 30
30
154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, (Rel. 35, 16) (Rel. 39, 16) C PROTEIN (18)
         N.A.
AND SPINAL CORD
                                                                                                                                                                                                  80
                                                                                                                                                                                                                       93
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35, Created)
                                                                                                                                                                                                                                                                                                          protein; Acetylation; Phosphorylation
0 BY SIMILARITY.
1 ACETYLATION (BY SIMILARITY).
30 K -> Q.
30 K -> R.
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1
30
30
16451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salerno
                                                                                                                                                                                                                                                       .08;
                                                                                                                                                                                                                                                                                                  W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC SIDE C
                                                                                              sequence up
annotation
                                                                                                                                                                                                                                            Score 8; DB 1; Pred. No. 0.4
0; Mismatches
                                                                                                                                                                                                                                             0
                                         : Craniata;
Squalea; So
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erinacia.
                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S., Saa
n basic
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sic proteins in
                                                                                                          update)
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                                                                                                                                           154
                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                         ı; Vertebrata;
Squaloidei; So
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                                                                                                                                           ₿
                                                                                                                                                                                                                                                     .45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF MYELIN.
C PROTEIN FAMILY.
                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                               Length 154;
                                         Squalidae;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gould R.M.
the shark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chondrichthyes;
Pristiorajea;
                                                  Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
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RESULT
PCP3_AN
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Best Local S
Matches 8
                                                                                                                                                                                                                       MEDLINE; 96413510.

Sharples F.P., Wrench P.M., Ou K., Hiller K.U., Proposed F.P., Wrench P.M., Ou K., Hiller K.U., Proposed F.P., Wrench P.M., Ou K., Hiller K.U., Proposed F. Peridinin-chlorophyll a-F.

Typo distinct forms of the peridinin-chlorophyll a-F.

Amphiddinium carterae.",

Biochim. Biophys. Acta 1276:117-123(1996).

Biochim. Biophys. Acta 1276:117-123(1996).

FUNCTION: WARER-SOLUBLE ANTENNA FOR CAPTURE OF FUNCTION: WARER-SOLUBLE AND IN ANY METRIC CAPTURE OF FUNCTION RANGE. PERIDININ IS AN ASYMMETRIC CAPTURE OF FUNCTION RANGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET
MOD_RES
SEQUENCE
                                                                                 SITE
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                             PRT; 323 AA.

PCC3 AMPCA STANDARD; PRT; 323 AA.

P80483;

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PERIDININ-CHIOROPHYLL A BINDING PROTEIN 3 (PCP).

Amphidinium carterae (Dinoflagellate).

Eukaryota; Alveolata; Dinophyceae; Gymnodiniales; Gymnodiniaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U44052; AAA96757.1; -. PFAM; PF01669; Myelin_MBP; 1. PRINTS; PR00212; MYELINMBP. PROSITE; PS00569; MYELIN_MBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94016687.

Spivack W.D., Zhong N., Salerno S., Saavedra R.A.

"Molecular cloning of the myelin basic proteins
acanthias, and the ray, Raja erinacia.";

Neurosci. Res. 35:577-584(1993).

-I- FUNCTION: THIS PROTEIN MAX FUNCTION TO MAINT
OF MYELIN.
                                                                                                                            Light-harvesting polypeptide; SITE 70 70 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF -!- SIMILARITY: BELONGS TO THE MYELIN BASIC PI
                                                                                                                                                                                       -1- SUBUNIT: HOMOTRIMER
-1- DOMAIN: THE MATURE
                                                                                                                                                                                                                                                                                                                                                                                  Amphidinium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myelin; Structural protein; Acetylation; Pl
INIT_MET 0 0 BY SIMILARITY
                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 PVVHFFKN
                                                                                                                                                                                                                     BLUE-GREEN RANGE. PERIDININ IS AN AMMAXIMUM ABSORPTION AT APPROXIMATELY
                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVHFFKN
                                                                                                                                                             P80484; 1PPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
8; Conserv
                                                                                                                                                                      UNITS
                                                                   174
323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
                                                                                                   244
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                   AA;
                                                                                    244
173
323
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16479
                                                                   34230 MW;
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                                                                                                                                                                                         PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salerno S., Saavedra R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                           , Ou K., Hiller R.G.;
peridinin-chlorophyll a-protein
                                                                                                                                                                                                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8; DB 1
: Pred. No. 0.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                           CHLOROPHYLL A-
CHLOROPHYLL A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACETYLATION (BY SII
; C129F8A824ABBC93
                                                                                    N
                                                                   478FB2DE2E3E2343 CRC64;
                                                                                                                                                                                                                                                                                                                                                      PARTIAL
No.
                                                                                                                                                                                       COMPOSED OF 2 ALMOST IDENTICAL
                                                                                                           st; Multigene
L A-BINDING.
L A-BINDING.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                 OF SOLAR ENERGY IN THE CAROTENOID HAVING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gould R.M.;
the shark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPER
                                                                                                                                            family; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
;
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Query Match Best Local

Similarity

4.7%;

Score Pred.

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RESULT 13

MBP_HETER

AC P2093

DT 01-FE
DT 01-FE
DT 01-FE
DT 01-FE
DT 01-FE
DT 15-FE
DT 15-FE
DT 15-FE
DT 15-FE
DT 15-FE
DT 11-FE
DT 11-F
  YG3Y_YEAST
ID YG3Y_Y
AC P53295
DT 01-007
DT 01-007
DT 15-JUI
DE HYPOTE
GN YGR177
OS Sacchk
OC Eukar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                        YG3Y_YEAST STAN
P53295;
O1-CCT-1996 (Rel. 3
O1-CCT-1996 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991
01-FEB-1991
15-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 90040744.

Saavedra R.A., Fors L., Aebersold R.H., Arden B., Ho Sanders J., Hood L.;

"The myelin proteins of the shark brain are similar proteins of the mammalian peripheral nervous system. J. Mol. Evol. 29:149-156 (1989).
-I- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Neoselachii; Galeomorphii; Heterodontoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYELIN BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X17664; CAA35661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heterodontiformes; Heterodontidae; Heterodontus.
     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
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T 0 0 BY SIMILARITY

O ACTULATION (BY SIMILARITY).

1 1 1 ACTULATION (BY SIMILARITY).

E 154 AA; 16502 MW; A9A57DA149429A83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Su G.L., Freeswick P.D., Geller D.A., Wang Q., Shapiro R.A., V Billiar T.R., Tweardy D.J., Simmons R.L., Wang S.C.; "Molecular cloning, characterization, and tissue distribution lipopolysaccharide binding protein. Evidence for extrahepatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein;
NP_BIND 70 7
NP_BIND 116 12
NP_BIND 250 25
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                                                                                                                                                                                                                                                                     FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL LIPODOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS TO INTERACT WITH THE CD14 RECEPTOR.
SIMILARITY: BELONGS TO THE BPI/CETP/LBP/PLTP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    Immuno1.
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P17213; 1BP1.
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ein; GTP-binding.
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D144569C9C5D777C CRC64;
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                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993).
EMBL; L18866; AAA72011.1; -.
PROSSITE; PS00569; MYELL, MEP; 1.
PRINTS; PR00212; MYELLNMBP.
SEQUENCE 304 AA; 33117 MW; 4E98BOAE CRC32;
                                                                                                                                                                                                                                                                                           MEDIJIE; 94068468.

MEDIJIE; 94068468.

PRIBYL T.M., CAMPAGNONI C.W., KAMPF K., KASHIMA T., HANDLEY V.W.,

MCMAHON J., CAMPAGNONI A.T.;

"The human myelin basic protein gene is included within a 179-kilobase

**ranscription unit: expression in the immune and central nervous
                                                                                                                                                                                                                                                                                                                                                                                                      HOMO Sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Primates; Catarrhini; Hominidae; Homo.
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             121 GQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR 171
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ilarity 100.0%;
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Pred. No. 4.6e-175;
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Q15339;
Q1-NOV-1996;
Q1-NOV-1996;
Q1-NOV-1998;
                       Q9Z1J5
Q9Z1J5;
Q1-MAY-1999
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Q9Z1J6;
Q1-MAY-1999
Q1-MAY-1999
Q1-NOV-1999
                                                                                                                                                                                                                                                                                                                                                    STRAIN-LEWIS RAT;
LOBELL A.M., WIGZELL H.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ132896; CAA10805.1; -.
PROSITE; PS00569; MYELIN_MBP; 1.
SEQUENCE 154 AA; 17207 MW; F3971E0B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJINE, 94068468.
MEDIJINE, 94068468.
MEDIJINE, GAMPAGNONI C.W., KAMPF K.
MCMAHON J., CAMPAGNONI A.T.,
"The human myelin basic protein gene i
01-MAY-1999
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Eukaryota; Metazoa;
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L18865; AAA72010.1; -.
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46; Conserv
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F3971E0B CRC32;
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Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                           Q61836 PRELIMINARY; PRT;
Q61836;
Q1.NOV-1996 (TIEMBLITEL 01, Last sc
Q1-NOV-1996 (TIEMBLITEL 12, Last sc
Q1-NOV-1999 (TIEMBLITEL 12, Last ar
MYELIN BASIC PROTEIN (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranj
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Q9Z1J4;
Q9Z1J4;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IOBELL A.M., WIGZELL H.;
submitted (FEB-1999) to the EM
EMBL; AJ132898; CAA10807.1; -.
PROSITE; PS00559; MYZLIN_MBP;
SEQUENCE 195 AA; 21484 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOBELL A.M., WIGZELL H.;
submitted (FEB-1999) to the EN
EMBL; AUI32897; CAA10806.1; -.
PROSITE; PS00569; MYELLN_MBP;
SEQUENCE 169 AA; 18470 MW;
                                                              SEQUENCE FROM N.A. STRAIN=C57BL/6J; T MEDLINE; 87118269.
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Eukaryota; Metazoa; Chordata; Craniata; Vei
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                     NEWMAN
                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
   NEWMAN S., KITAMURA K., CAMPAGNONI A. 
"Identification of a cDNA coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                        Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.) (TrEMBLrel.)
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llarity 100.0%;
Conservative
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                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                  Chordata; Craniata;
Sciurognathi; Murida
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Last sequence update)
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Pred. No. 2.1
0; Mismatches
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B0A7C0A0 CRC32;
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79E52D9D CRC32;
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fifth
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2.3e-41;
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2.1e-4;
                                                                                                                                                                                  Vertebrata;
ae; Murinae;
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ae; Murinae;
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   of myelin
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update)

Mammalia; Mus.

KAMPF K., IS., GARBAY

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RESULT
Q03139
ID Q0
AC Q0
DT .01
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Best Local S
Matches 34
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Best Local
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Proc. Natl. Acad. Sci. U.S.A. 84:8
EMBL; M15062; AAB59712.1; -.
PROSITE; PS00569; MYELIN_MBP; 1.
Alternative splicing; Myelin.
NON_TER 1
SEQUENCE 149 AA; 16226 MW; A6D
Q03139 PRELIMINARY;
Q03139;
.01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN. EMBL; X67319; CAA47733.1; -. EMBL; X67319; CAA4773721.1; -. EMBL; L07508; AAA37721.1; -. MGD; MGI:96925; Mbp.
MGD; Structural protein; Acetylation; Methylation; Myelin; Structural protein; Acetylation; Structural protein; Alternative splicing. SEQUENCE 195 AA; 21004 MW; 557D83EA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain.";
J. Biol. Chem. 268:4930-4938(1993).
-i- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57 BLACK; TISSUE-BONE MARROW; MEDLINE; 93057537.

GRIMA B., ZELENIKA D., PESSAC B.;

"A novel transcript overlapping the m
J. Neurochem. 59:2318-2323(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
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MEDLINE; 93186801.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                       SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 46
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                                                                                                                                                                                                                        19.9%;
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; Pred. No. 1.3;
0; Mismatches
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   Created)
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Pred. No.
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S., GARBAY B.,
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                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
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RESULT
P87346
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Q61837
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Best Local S
Matches 34
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O61837 PRELIMINARY; PRT; 34 AA. 051837; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1999 (TrEMBLrel. 01, Last sequence up 01-NOV-1999 (TrEMBLrel. 12, Last annotation MYELIN BASIC PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                          Myelin.
NON_TER
NON_TER
SEQUENCE
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MEDLINE; E
OKANO H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene that encompasses the myelin basic protein gene an in cells in the oligodendrocyte lineage in the brain."
J. Biol. Chem. 268:4300-4938(1993).

EMBL; LO7507; AAA37720.1; -.

PRINTS; PRO0212; MYELINMBP.
Myelin; Structural protein; Acetylation; Methylation; Autoimmune encephalomyelitis; Alternative splicing.
SEQUENCE 250 AA; 27167 MW; 3A08ADE7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-BRAIN;
MEDLINE; 93186801.
CAMPAGNONI A.T., PRIBYL T.M.,
AMUR-UMARLEE S., LANDRY C., H
                                                                                                                                                                                                                                                                                                                                                                   EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                        "Gene organization and transcription deficient (shi(mld)) mutant mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).

Riikarvota; Metazoa; Chordata; Craniata; Vertebrata;

Riikarvota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01.NOV-1996 (TIEMBIrel. 01, Last sequence update) 01.NOV-1999 (TIEMBIREL. 12, Last annotation updat MYELIN BASIC PROTEIN (MPB).
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                    EMBL; M36275;
                                                                                                                                                                                                                                                                                                                                                                                                                            MIKOSHIBA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KITAMURA K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and developmental regulation of Golli-mbp, a 105-kilobase gene that encompasses the myelin basic protein gene and is expressed in cells in the oligodendrocyte lineage in the brain.";
                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                       HGRTQDENPVVHFFKNI
                                                                                                                                                              l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                     nt (shi(mld))
7:77-83(1988)
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88196094.
                                                                                                                                                                                                                                                                                                                                     PS00569;
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                                                                                                                                                                                                                                                          34 AA;
                                                                                                                                                                Conservative
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 PRELIMINARY;
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569; MYELIN_MBP;
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%; Pred. No. 2e-
0; Mismatches
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                                                                                                                                                                0;
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Pred. No.
                                                                                                                                                                                                                                                          31F53967 CRC32;
PRT;
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                                                                                                                                                                Mismatches
176
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177

update) update)

DB 11; 2e-28;

Length

Phosphorylation;

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Indels

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Gaps

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DB 11; 6e-11;

Length

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Indels

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IKENAKA K.,

OSHIMURA M.,

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Best Local 9
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01-MAY-1997 (TrEMBLrel. (
01-MAY-1997 (TrEMBLrel. (
01-NOV-1999 (TrEMBLrel. )
MYELIN BASIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q38690
Q38690;
01-NOV-1996
01-NOV-1996
01-NOV-1999
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01-NOV-1996
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 12, Last annotation update)
HIGH SALT PERIDININ-CHLOROPHYLL A-PROTEIN (FRAGMENT).
Amphidinium carterae (Dinoflagellate).
Amphidinium carterae (Dinophyceae; Gymnodiniales; Gymnodiniaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myelin.
SEQUENCE
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Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHARPLES F.P., WRENCH P.M., OU K., Blochim. Blophys. Acta 0:0-0(1996) EMBL; Z71600; CAA96255.1; -
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"CDNA for Xenopus laevis myelin
Submitted (JAN-1997) to the EMBI
EMBL: AB000736; BAA19174.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-J; TISSUE-BRAIN;
NAGATA S., OGINO K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve:
Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                  Human herpesvirus
                                                                                                                                                                                                                                                    Q69559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MENDEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CS
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Similarity 100.0%
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16839;
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8; Conserv
                    dsDNA viruses,
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281
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                                                                                                                             (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
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                                                  <u>ი</u>
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29946 MW;
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Last sequence
Last annotation
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Last sequence update)
Last annotation updat
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Pred. No. 1.6
0; Mismatches
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EMBL/GenBank/DDBJ databases
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Pred.
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                 stage; Herpesviridae;
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ea; Pipidae;
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Xenopodinae;
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OR GROED REPERD OR OR GROED REPERD OR GROED GROE
SEQUENCE FROM N.A.
STRAIN-U1102, VARIANT A;
MEDLINE; 93091236.
GOMPELS U.A., CARSS A.L., S
"Infectivity determinants e
herpesvirus-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-U1102, VARIANT A;
MEDLINE; 91237802.
CHANG C.K., BALACHANDRAN N.;
"Identification, characterization,
encoding a phosphoprotein of human
J. Virol. 65:2884-2894(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95266321.
GOMPELS U.A., NICHOLAS J.,
MARTIN M.E., EFSTATHIOU S.,
"The DNA sequence of human
and genome evolution.";
                                                                                                                                                                                           GENG Y., CHANDRAN B., JOSEPHS S.F., WOOD C.; "Identification and characterization of a human herpesvirus 6 segment that trans activates the human immunodeficiency virus
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-U1102, VARIANT
MEDLINE; 92148942.
GENG Y., CHANDRAN B.,
                                                                                                                                                                                                                                                                                                                                                rIGENTATHIOU S., LAWRENCE G.L., BROW "IGENTIFICATION of homologues to t family in human herpesvirus 6.", J. Gen. Virol. 73:1661-1671(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-U1102, VARI
MEDLINE; 92333249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THOMSON B.J., EFSTATHIOU S., HONESS R.W.;
"Acquisition of the human adeno-associated human herpesvirus type-6.";
Nature 351:78-80(1991).
[6]
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STRAIN-UI102, VARIANT A;
STRAIN-UI102, VARIANT A;
MEDILINE; 90080132.
LAWRENCE G.L., CHEE M., CRAXTON M.A., GC
BARRELL B.G.;
"Human herpesvirus 6 is closely related
J. Virol. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a transactivating function mapping immediate-early locus of human herpesvirus 6.";
J. Virol. 65:5381-5390(1991).
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MARTIN M.E.D., NICHOLAS J.,
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STRAIN-U1102, VARIANT
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LIU D.X., GOMPELS U.A., FOA-TOMASI L., CAMPADELLI-FIUME G.;
"Human herpesvirus-6 glycoprotein H and L homologs are components
the gpl00 complex and the gH external domain is the target for
neutralizing monoclonal antibodies.";
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H and interaction with an accessory 40K glycoprotein.";
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SEQUENCE FROM N.A.
THING, VARIANT
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J. Virol. 66:3918-3924(1992).
"Identification and mapping of complex gp82-gp105 of human her neutralizing epitope recognized J. Virol. 67:4611-4620(1993).
                                                                  SEQUENCE FROM N.A.
STRAIN-U1102, VARIANT
MEDLINE; 93323202.
                                                                                                                                and mapping
                                                                                                                                    GREENAMOYER C., DAMBAUGH T.R.;

A Strongly immunoreactive virion protein of human herp
variant B strain Z29: identification and characterizati
and mapping of a variant-specific monoclonal antibody r
                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-U1102, VARIANT MEDLINE; 93331710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The right end of the unique region of UllO2 contains a candidate immediate homologue of the human cytomegalovirus J. Gen. Virol. 73:1649-1660(1992).
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STRAIN-U1102, VARIANT A;
STRAIN-U1102, VARIANT A;
MEDLINE; 94202884.
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herpesvirus 6 genome.";
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SEQUENCE FROM N.A.
STRAIN-U1102, VARIANT A;
MEDLINE; 95146989.
GOMPELS U.A., MACAULAY H.A.
GOMPELS U.A., MACAULAY H.A.
SEQUENCE FROM
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ISEGAWA Y., MU
SUNAGAWA T., S
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J. Virol. 67:7680-7683(1993).
                                                                                                                   Betaherpesvirinae;
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J. Gen. Virol. 76:451-458(1995).
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ENKEL N., ROSENTHAL L.J.;
transforming fragment within the
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MUKAI T., NAKANO K., KAGAWA M., CHEN J., MORI Y
, SASHIHARA J., ZOU P., KOSUGE H., YAMANISHI K.;
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Best Local Similarity
Matches 7; Conser
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Best Local :
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MEDLINE: 98044033.

MEDLINE: 98044033.

KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,

RZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,

BORRISS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,

BOUTILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,

CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,

DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMMERSON P.T.,

ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,

TRATTS C., FUJITA M., FUJITA Y., FUMA S., GALLIZZI A., GALLERON N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     031793;
031793;
01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94118404.

MICHOLAS J., MARTIN M.;

"Nucleotide sequence analysis of a 38.5-kilobase-pair region of genome of human herpesylrus 6 encoding human cytomegalovirus immediate-early gene homologs and transactivating functions.";

J. Virol. 68:597-610(1994).

EMBL; L25528; AAA16731.1; -

SEQUENCE 93 AA; 10834 MW; BB463ABE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q69048;
Q69048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 variant A and B.";
J. Virol. 0:0-0(1999).
EMBL; AB021506; BAA78245.
SEQUENCE 88 AA; 10237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herpesvirus 6.
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7; Conserva
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3 (TrEMBLrel.
4 (TrEMBLrel.
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 08, Last annotation update)
6 IMMEDIATE-EARLY GENE HOMOLOGUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.18;
ilarity 100.08;
Conservative
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus/Clostridium us group; Bacillus.
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05, Last sequence update)
08, Last annotation update)
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Pred. No. 7.2
0; Mismatches
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Pred. No.
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lo. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12;
b. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
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RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KURITA K., LAPIDUS A., LANDINGIS S., LAUBER J., LAZAREYIC V.,
RA KURITA K., LAPIDUS A., LARDINGIS S., LAUBER J., LAZAREYIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
RA NOONE D., O'REILLY M., PORTETELLE D., PORMOLLIK S., PRESCOTT A.M.,
RA PRESECAN E., PUJIC P., PURNELLE B., ROCHE B., ROSE M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA RIEGER M., RIVOLTA C., ROCHA E., SCHROETER R., SCOFFONE F.,
SOROKIN A., TACCONI E., TAKAGI T., TERPSTRA P., SCHNOI A.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA VIANI A., WAMUTT R., WEDLER E., WEDLER H., WEITZENEGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA VOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KUNST F., ÓGASAWARA N., YOSHIKAWA H., DANCHIN Submilted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL, Z99113; CAB13615.1; -. SEQUENCE 123 AA; 13781 MW; C48C6BF8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                123
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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0; Mismatches
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databases
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Search information block:
Query: US-09-218-277-12
Query: Ingth: 171
Database: EST:*
Database sequences: 5247842
Database length: -2090053206
Search time (sec): 616.770000
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9b_est29:AU035929
9b_est29:AU051010
9b_est29:AU05101763
9b_est29:AU051763
9b_est29:AU051764
9b_est29:AU051764
9b_est29:AU050589
9b_est29:AU080007
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gb_est28:AL037973
gb_est29:AU079802
                       9b_est29:AU080202
9b_est29:AU080310
9b_est29:AU080356
9b_est29:AU080187
9b_est29:AU0807954
9b_est29:AU079655
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gb_est29:AU067431
gb_est29:AU051764
gb_est29:AU035931
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Sequence
                                                                                                                                                                                                                                                                                                                               gb_est5:AA325654
gb_est29:AU050919
                                                                                                                                                                                                                                                                                                                                                                  gb_est29:AU066968
gb_est28:AU035326
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est6:AA352612
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gb_est45:AW669230
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gb_est29:AU079452
                                                                                                                                                                                                                                                                                                 gb_est5:AA323848
                                                                                                                                                                                                                                                                                                                 gb_est10:AA683007
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est18:AI2723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est29:AU080522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgnl_1/USPTO_spool/US09218277/runat_26092000_140042_3783/app_query.fasta_1.231
-DB-EST -QEMT-fastap -SUFTX-rst -GAPOP=12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -QGAPOP=4.500
-QGAPEXT-0.050 -XGAPOP=10.000 -XGAPEXT-0.500 -FGAPOP=6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALION-200 -THR_SCORE-pct -THR_MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-2000000000 -USER-US09218277_@CCM1_1856 -NCPU-6
-ICPU-3 -LONGLOG -NO_XLPXY -WAIT -THREADS-1
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US-09-218-277-12 x AW657586
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gb_est29:AU079134
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gb_est29:AU067300
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Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 77 row: I column: 2
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
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1 (bases 1 to 573)
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Design and use of four pooled
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MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                              /organism="Bos taurus"
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/lab_host="DH10B"
   841.00
5.036
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                                                                                                               /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: Library made from pooled tissue from lymph node, c fat, hypothalamus, and pituitary."

195 c 171 g 82 t
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Length: 173
Gaps: 2
Identity: 91.329
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seq_documentation_block:
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                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Canc Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Braunschweig/Germany) within the cDNA sequencing consortium o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL037973 526 bp mRNA ES
DKFZp564P227_r1 564 (synonym: hfbr2) Homo
DKFZp564P227 5', mRNA sequence.
                                                                                                                       No s1 sequence available.
This clone (DKFZp564P227) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                On Oct 6, 1998 this sequence version replaced Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 526)
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Unpublished (1999)
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EST.
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/clone="DKRZP564P227"
/clone_lib="564 (synonym: h
/tissue_type="brain"
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Ratio:
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 808)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, & Suzuki, Y., Sasaki, M. and Sugano, S.
                                                                                                                                                                                                               AU079802 Sugano mouse brain mncb Mus musculus 5', mRNA sequence.
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/lab_host="X1-2blue"
/note="Vector: pAMP1;
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                                                                                                                                                                        GI:6084557
                                                                                                                                                                                                                                                     dq 808
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82 t
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0
99.355
                                                             Muridae;
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117

361

311 84 261 67 50

211

111 17

411

511

461

REFERENCE AUTHORS

COMMENT

source

cDNA clone MNCb-4774

Ito, A.,

Euteleostom1; Murinae; Hirata, M.,

TITLE JOURNAL

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

539

165

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alignment_block:
US-09-218-277-12 x AU079802
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ORIGIN
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                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                      34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 CACAGCAAGTACCATGGACCATGCCAGGCATGGCTTCCTCCCAAGGCACA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                                   aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA 83
                                                                                                                                                                                                                                                                                                                                                              GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAGG
                                         ProProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSe 116
                                                                                                                                                                                TACCCATTATGGCTCCCTGCCCCAGAAGTCGCAGCACGGCCGGACCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGCATCACAGAAGAGACCCTCACAGCGA....TCCAAGTACCTGGC 92
                                                                                                                                                                                                                                                                      GGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC....ACGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method Unpublished (1999) On May 18, 1998 this sequence version replaced gi:3137154. Contact: Katsuyuki Hashimoto Division of Genetic Resources National Institute of Infectious Diseases National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan Email: khashienih.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested and cloned into dstinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCTCTAAAACCTGCG]"

89 a 246 c 206 g 163 t 4 others
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4.964
96.532
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/lab_host="TOP10"
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/sex="female"
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/clone="MNCb-4774"
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/strain="C57BL"
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BASE COUNT
ORIGIN
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AUTHORS
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SOURCE
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VERSION
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LOCUS AU050833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACTATAAATCGGCTCACAAGGGATTCAAGGGGGCCTACGACGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 811)
Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K., Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
Construction of mouse full length-enriched cDNA libraries by
                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Oct 30, 1998 this sequence version replaced gi:3816313
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU050833 Sugano mouse brain mncb 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                     Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/
Seq primer: 5' end primer: CTTCTGCTCTAAA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligo-capping
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo
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                199
                         /db_xref="taxon:10090"
/clone="MNCb-1114"
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/strain="C57BL"
                                                                                                                                                                                                                                          /sex-"female"
                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                         dev_stage="adult"
               224 c
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             211 g
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                                                                                                                                                                                                                                                                                                                                                                       CTTCTGCTCTAAAAGCTGCG
             164 t
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             13 others
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alignment_scores

Percent Similarity:

Quality: Ratio:

821.00 4.946 95.954

Length: 173
Gaps: 4
Percent Identity: 93.064

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SOURCE
ORGANISM
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LOCUS AU079452
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US-09-218-277-12 x AU050833
                                                                                                                                                                                                                                                         KEYWORDS
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                                                                                                                                                                        REFERENCE
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                                                                                        JOURNAL
                                                                                                                         TITLE
                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 GlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGl 165
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Suzuki,Y., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M., Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method

Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3136677.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
National Institute of Infectious Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCACGCTTTCCAAAATCTTTAAGCTGGGAGGAAGAGACAGCTGCTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC....ACGAGAAC
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                                                                                                                                                                                                                                                                                      AU079452 Sugano mouse brain mncb 5', mRNA sequence.
AU079452
                                                                                                                                                                                                                      Mus musculus
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alignment_block:
US-09-218-277-12 x AU079452
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Percent Similarity:
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285
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                                                                                                                                                                                                                                                                                                                                                                                               47 ATGGCATCACAGAAGAGACCCTCACAGCGA.....TCCAAGTACCTGGC
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                                                                                                                                                                                                                                                                                                                rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg
                                                               rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaS
                                                                                                                         ProProProSerGinGlyLysGlyArgGlyLeuSerLeuSerArgPheSe 116
                                                                                                                                                   ATGAAAACCCAGTAGTCCATTTCTTCAAGAACATTGTGACACCTCGAACA
                                                                                                                                                                                                    TACCCATTATGGCTCCCTGCCCCAGAAGTCGCAGCACGGCCGGACCCAAG
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4.946
95.954
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/strain="C57BL"
/db_xref="taxon:10090"
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/lab_host="TOP10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 173
Gaps: 4
Percent Identity: 93.064
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US-09-218-277-12 x AU067209
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Isolation of full-length cDNA clones from a mouse brain cDNA library made by oilgo-capping method Unpublished (1999)
On Jul 9, 1999 this sequence version replaced gi:5434934.
Contact: Katsuyuki Hashimoto Division of Genetic Resources National Institute of Infectious Diseases National Institute of Infectious Diseases
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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5', mRNA sequence.
AU067209
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Email: khashi@nih.go.jp/yoken/genbank/.
URL: http://www.nih.go.jp/yoken/genbank/.
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96.450
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                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
E 1 (bases 1 to 720)

KS Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oilgo-capping method
Unpublished (1999)
On Oct 8, 1998 this sequence version replaced gi:3727975.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashimoto
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
1 720
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5', mRNA sequence.
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    brain
  mncb"
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165

clone MNCb-3446

482 148 432 133

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67 188 50

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alignment_block:
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Gaps: 5
Percent Identity: 92.529
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SOURCE
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US-09-218-277-12 x AU051764
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Percent Similarity:
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142 GAGACACGGGCATCCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAGG
               34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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                                                                                        aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
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URL: http://www.nih.go.jp/yoken/genbank/
Seq primer: 5' end primer: CTTCTGCTCTAAAAGCTGCG.
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Sasaki, M., Suzuki, Y., Watanabe, M., Imai, J., Shibui, A., Yoshida, K., Hata, H., Yamaguchi, R., Tateyama, S. and Sugano, S. Construction of mouse full length-enriched cDNA libraries by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU051764 800 bp mRNA EST 18-MAR-1999
AU051764 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2446
5', mRNA sequence.
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Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1 chome, Shinjuku-ku, Tokyo
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On Feb 22, 1999 this sequence version replaced gi:4283685
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92.529
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seq_documentation_block:
LOCUS AU035931
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                                                                                                                                                                                                                                                                                         ESM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

CE 1 (bases 1 to 779)

RS Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,

Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.

Construction of mouse full length-enriched cDNA libraries

Unpublished (1998)

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National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan

Email: khashienih.go.jp.
Location/Qualifiers
1 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Phote-"Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG] , digested and cloned into dstinct DraIII sites of the pME18S-FL3. XhoI sites just outside the DTAIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by
                                                                                                                                                  /dev_stage="adult"
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                                                                                                                                                                                   /clone_lib="Sugano mouse
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                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="MNCb-1058"
                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL"
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clone MNCb-1058
                                                      ACCESSION
VERSION
KEYWORDS
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ORIGIN
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Quality:
Ratio:
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                                       SOURCE
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                                                                                                                                 DEFINITION
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|CTGGGGGGCCGAGGGCAGAAGCCAGATTTGGCTACGGAGGCAGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spGluAsnProValValHisPhePheLysAsnIleValThrProArgThr 99
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                                                                                                                                                                                                                                        ATCTCCA 542
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                                                                                                       AU051348 804
AU051348 Sugano mo
5', mRNA sequence.
   Mus musculus
Eukaryota; M
                                                                          AU051348.1 GI:4434357
                                                                                             AU051348
                                       house mouse.
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223 c 203 g 153 t 11 others
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4.790
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     Metazoa;
                                                                                                                                                804 bp
                                                                                                                             mouse brain
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   Chordata;
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   Craniata;
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4
   Vertebrata;
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TITLE JOURNAL COMMENT

FEATURES

18-MAR-1999 CDNA clone MNCb

MNCb-1908

Euteleostomi;

165 486 148 436 133 386

REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION

149

142 50

92

192

236

436 133

536 165 386

116

336

100 286 236

67

83

192

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BASE COUNT
ORIGIN
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AUTHORS
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                        spGluAsnProValValHisPhePheLysAsnIleValThrProArgThr
                                                                                                                 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA
ATGAMAACCCAGTAGTCCATTTCTTCAAGAACATTGTGACACCTCGAACA
                                                                                         TACCCATTATGGCTCCCTGCCCCAGAAGTCGCAGCACGGCCGGACCCAAG
                                                                                                                                                                                  GGTGCGCCCAAGCGGGGCTCTGGCAAGGACTCACAC....ACGAGAAC
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Ratio:
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Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K., Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S. Construction of mouse full length-enriched cDNA libraries by oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
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On Jun 5, 1998 this sequence version replaced gi:3187684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG] , digested and cloned into dstinct DraIII sites of the pME18S-FL3. xhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGCG]"

90 a 204 c 176 g 176 t 58 others
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93.103
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/clone="MNCb-1908"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="Sugano mouse brain mncb"
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Gaps: 5
Percent Identity: 89.080
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alignment_scores:

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JOURNAL COMMENT
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LOCUS AU066815
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
El (bases 1 to 771)
S Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA
Library made by oligo-capping method
Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3036368.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1. Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashighinh, go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AU066815 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-2602 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU066815.1 GI:4967552
                187
              þ
                                       /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-2602"
                                                                                                                                                                                                                                                                    /clone_lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                       'lab_host="TOP10"
                                                                                                                                                                                                                                        'dev_stage="adult"
                                                                                                                                                                                                                                                           'sex="
                                  CTTCTGCTCTAAAAGCTGCG]"
              219 c
                                                                                                                                                                                                                                                          female"
              14 others
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DEFINITION
ACCESSION
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                                                                                    REFERENCE
AUTHORS
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LOCUS AW669230
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US-09-218-277-12 x AU066815
                                                                                                                                                                                                                                                                                                         seq_name: gb_est45:AW669230
                                                                                                                                                                               SOURCE
                                                                                                                                                                                               EYWORDS
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                                    TITLE
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      JOURNAL
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{|||||||||||:::::
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                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bov. 1 (503) Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A. and Keele, J.W.
                                                                                                                                                                                                                                          AW669230 503
112503 MARC 1BOV B
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                                                                                                                                                                                                                               AW669230
                                                                                                                                                              Bos taurus
                                                                                                                                                                               Bos taurus.
                                                                                                                                                                                                              AW669230.1
    Unpublished (2000)
                     Design and use of four pooled tissue EST discovery in cattle
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US-09-218-277-12 x
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133 erAspTyrLysSerAlaHisLysGlyPheLysGlyVal...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetalaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl
                                                                   rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaS
                                                                                                           CTCCCCCATCTCAAGGGAAGGGCCAGGACTGTCCCTCANCAGATTTAG
                                                                                                                           ProProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSe
                                                                                                                                                                        GAGACACTGGCATCCTCGACTCCCTCGGCCGCTTCTTTGGCGCTGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCCGCGAGCACCATGGACCACGCCACGCCTTCCTTCCCAGGCACA
                                                                                                                                                                                                                                                                                                       GGTGCGCCCAAGCGGGCTCGGGCAAGGATGGACACCACGCGGCCAGGAC
                                                 CTGGGGCGCCGAGGGCCAGAAGCCGGGATTCGGCTACGGAGGCAGAGCTC
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jul 8, 1999 this sequence version replaced g1:5422693. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366

Fax: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 105 row: D column: 18 Seq primer: ATTTAGGTGACACTATAG
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
171 c 148 g 71 t 1 others
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96.226
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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US-09-218-277-12 x AU080522
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                                                                                                                                                                           Align seg 1/1 to: AU080522
                                                                                                                                                                                                                                                                                      Percent Similarity:
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 782)

1 (bases 1 to 782)

Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,

Suzuki,Y., Sasaki,M., and Sugano,S.

Suzuki,Y., Sasaki,M., and Sugano,S.

Suzuki,T., Sasaki,M., and Sugano,S.
                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library made by oligo-capping method Unpublished (1999)
On Jul 7, 1999 this sequence version replaced Contact: Katsuyuki Hashimoto
Division of Genetic Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-1, Toyama 1-chome, Shinjuku-ku, Tokyo
Email: khashi@nih.go.jp/yoken/genbank/.
URL: http://www.nih.go.jp/yoken/genbank/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo
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                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-Torgan: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a Drail adaptor [TGTTGGCCTACTGG], digested and cloned into dstinct Drail sites of the pME18S-FL3. Xhor sites just outside the Drail sites can be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTGCTCTAAAAGCTGCG]]
                                                                                                                                                                                                                                                                                  753.00
4.827
93.976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-5756"
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/lab_host="TOP10"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 GlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSer 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 NCGACTATAAATCGGNTCACAAGGGATTCAAGGGGGCCTACGACGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 CCACCTCCATCCCAAGGGAAGGGGAGAGGCCTGTCCCTCAGCAGATTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 TACCCATTATGGCTCCCTGCCCCAGAAGTCGCAGCACGGCCGGACCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 GGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC....ACGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA 83
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                                                                                                                                                                                                                                                                             Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3036477.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp/yoken/genbank/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 770)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M., Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by Oligo-capping method
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/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTT] double-stranded cDNA was
                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL"
                                                                   /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                    /clone_lib="Sugano mouse
/sex="female"
                                                                                                                                                                  /db_xref="taxon:10090"
/clone="MNCb-2726"
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alignment_block:
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                                                                                                                                                                                                                                GlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGl
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                                                                                                                                                                      ySerProMetAlaArgArg 171
                                                                                                                                                                                                           GGCACGCTTTCCAAAATCTTTAAGCTGGGAGGAAGAGACAGCCGCTCTGG
                                                                                                                                           ATCTCCCATGGCGAGACGC
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Ratio:
            AA352612 511 bp mRNA EST EST60632 Activated T-cells XX Homo sapiens myelin basic protein, mRNA sequence.
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90.173
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                               similar to
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VERSION
KEYWORDS
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Quality:
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Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                     aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
                                                                                                                                                                              ATGGCGTCACAGAAGACCCTCCCAGAGGCACGGNTCCAAGTACCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taTCC (inhost):152811"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
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4.993
93.750
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Gaps: 2
Percent Identity: 89.375
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136 GAGACACGGGCATCNTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAGG
                                              GGGGGCCGAANAGTAGNACCAGGATTTTGGCTACGGAGGCAGAGCGTCCG 435
                                                    pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                              Score
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASQKRPSQRHGSKYLATAS.....SKIFKLGGRDSRSGSPMARR 171
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R955406
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Rat myelin basic
Chicken myelin basic
Chicken myelin basic
Residues 139-170
Residues 139-170
Residues 131-135
Human myelin basic
Human myelin basic
Human myelin basic
MBP-2. 5 (80-104)
Human myelin basic
MBP-5 (101-125)
Human myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
             XXX
Human myelin basic protein (MBP).
Myelin basic protein; MBP; multiple sclerosis; MS;
inhibition; major histocompatability complex; MHC;
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ALIGNMENTS

RESULT R97627	1
g A	rst entry)
E	basic protein.
Z Z	protei analogu
8 20	Homo sapiens.
FH	1
日	tide 8699
	30-MAY-1996.
	16-NOV-1995; U14402.
	US-34:
	OSCIENCE
	268534/27. T30269
	numan myelin basic pro
	mino acid, useful to treat multiple scl
	omprising amino acids 87-99 of 1
38	be used to treat and prevent multiple
၁ ဇ	peptide analogue is administered at a dosage range of 5-50 mg/kg. Sequence 171 AA;
Qu Be	Query Match 100.0%; Score 922; DB 1; Length 171; Best Local Similarity 100.0%; Pred. No. 3.1e-90; Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	HARHGFLPRHRDTGILDSIGRFFGGDRGAPKRGSGF
ğ	1 MASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFGGDRGAPKRGSGKD 60
Qγ	61 SHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAE 120
망	61 SHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAE 120
Qy	121 GQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR 171
Дb	121 GQRPGFGYGGRASDYKSAHKGFKGYDAQGTLSKIFKLGGRDSRSGSPMARR 171
RESULT	ED 2
383	
	07-NOV-1996 (first entry) Human myelin basic protein (MRD)
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competition; thymocyte; T cell;

experimental allergic encephalomyelitis; EAE; analogue.

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30-MAY-1996.
16-NOV-1995; U14403.
18-NOV-1994; US-342408.
(NEUR-) NEUROCRINE BIOSCIENCES II
CODION DJ. GAUT A, Ling N, St.
WPI; 96-268535/27.
                                                                                                                                                                                                                                                                                                                     03-MAR-1994.
17-AUG-1993; U07-786.
17-AUG-1992; US-931217.
(AUTO-) AUTOIMMUNE INC.
Hafler DA, Weiner HL;
WPI; 94-082786/10.
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Reptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis

Disclosure: Figure 1; 61pp; English.

Deptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP peptide to MHC and by not causing proliferation of an MBP reactive cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents.
                                                    Myelin basic proteins (sequences R48592-96) and cattle proteolipid protein (R48592) elicit the release of TGF-beta from suppressor T-cells and target the T-cells to neural tissue under cytotoxic attack, thereby reducing neurological disease, e.g. HTLV-1 associated myelopathy, tropical spastic paraparesis and HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteolipid protein; myelin basic protein; retrovirus; neurological disease; by-stander antigen; TG:-beta; transforming growth factor-beta; T-cell; T-lymphocyte; myelopathy; paraparesis; human immunodeficiency virus type 1.
                                                                                                                                                                                                    Treating retroviral associated neurological disease - lof by stander antigen, causing release of transforming factor beta from suppressor T cells
Disclosure; Page 49; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-1994 (first entry)
Human myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
WO9404121-A.
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                              Infection.
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nes 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRESWGAE
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Steinman L;
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Query Match

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Similarity

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ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFGGDRGAPKRGSGKDS

ASQKRPSQRHGSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFGGDRGAPKRGSGKDS

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PA (LMNU), ASSAULT PER PI DEVAILE BY FRANCE H, Gefter M, HSU U, FRANCE PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Samson M, Shi J, Smilek D;
PI Rothbard J, Smilek D;
PI Ro
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W02-MAY-1996. U13682.

25-OCT-1995; U13682.

R 25-OCT-1994; US-328224.

PR 25-OCT-1995; US-404228.

PR 25-OCT-1995; ZA-00903.

PA (1MMU-) IMMULOGIC PHARM CORP.

Devaux B, Franzen H, Gefter M, J

Devaux B, Samson M, Shi J, Sm
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Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; Myelin basic protein; MBP; experimental allergic entral nervous system; CD4+; T-cell; autoimmune disease; demyelination; central nervous system; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP; diabetes; Graves disease; myasthenia gravis; GOO Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG; myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
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Best Local S
Matches 168
                                                                                                                                                   Homologous peptide analogues of human basic myelin protein - used for treating multiple sclerosis. Disclosure; Fig 4; 26pp; English. The sequence is that of human basic myelin protein (BMP). Fragment: of this sequence are claimed (see features) which are able to neutralise anti-BMP antibodies and are thus useful in treatment of multiple sclerosis. The fragments may be prepd. synthetically and avoids the dangers associated with the use of the natural protein, e.g. transmission of neuroviruses. Also the peptides are too small to be immunogenic.
                                                                                                                                                                                                                                                                                        29-APR-1993.
15-OCT-1992;
22-OCT-1991;
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WPI; 93-152422/18.
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                                          HHPARTAHYGSLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGKGRGLSLSRFSWGAEG
QRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKIFKLGGRDSRSGSPMARR
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multiple sclerosis;
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CA-053799.
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Matches 171; Conserv
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07-NOV-1996.
22-APR-1996; U05611.
22-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 79-80; 156pp; English.

The native human 21.5 kDa foetal isoform (W00399) of myelin basic protein, MBP+X2Cy881, includes an exon 2-encoded region (X2) that may contain an epitope involved in the pathogenesis of multiple sclerosis (MS); the X2 region is not found in the MBP of healthy adults. Recombinant MBP+X2, or variants modified to improve bacterial expression (see also W06107), can be produced in a large scale in bacterial hosts. They are useful for assaying T-cells for responsiveness to MBP epitopes and can be used as therapeutic agents that act by inducing T-cell responses, including anergy and apoptosis, as a means of treating MS. Sequence 197 AA;
W06107 standard;
W06107;
01-FEB-1997 (fir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALEX-) ALEXION PHARM INC.
(USSH ) US DEPT HEALTH & F
Lenardo MJ, Matis L, McI
Nye SH, Pelirey CM, Squir
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                                                                                                                                                                                                                        FKLGGRDSRSGSPMARR 171
                                                                                                                                                                                                                                                                                                      VTPRTPPPSQGKGRGLSLSRFSWGAEGQRPGFGYGGRASDYKSAHKGFKGVDAQGTLSKI 154
                                                                                                                                                                                                                                                                                                                                                                                                         -----KDSHHPARTAHYGSLPQKSHGRTQDENPVVHFFKNI 94
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amino acid, esp. an uncharged amino acid
of mol.wt. below below about 150, partic.
Ser, in constructs of the invention"
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Best Local S
Matches 171
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02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-431644.
07-JUN-1995; US-43114.
(ALEX-) ALEXION PHARM INC.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
WPISSA SH, Pelfrey CM, Squinto SP, Wilkins
WPI; 96-55898/50.
peptide
                                                                                                                                                                        01-FEB-1997 (first entry)
Foetal myelin basic protein; MBP+X2Ser81/bact.
Myelin basic protein; MBP, MBP+X2Ser81; prote
multiple sclerosis; autoimmune disease; diagn
T-lymphocyte; T-cell; anergy; apoptosis.
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A 21.5 kDa foetal isoform (W06107) of myelin basic protein, MBP+X2Cys81/bact., is the product of a DNA construct (T41896) based on the human foetal MBP+X2Cys81 isoform (W00399) but utilising bacterially-preferred codons in place of the native human codons (see also T41889). This increases prodn. of the MEP in E. coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also W00399 and W06108) are useful in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; T41896.
New human myelin basic
used in the assessment,
                                                                                                                                                                                                                                                                                                      W06108 standard; W06108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Foetal myelin basic protein MBP+X2Cys81/Dact.
Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein;
multiple sclerosis; autoimmune disease; diagnosis; therapy;
T-lymphocyte; T-cell; anergy; apoptosis.
                                                                                                                                                            Synthetic.
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              60. .85
/label= x2
/note= "exon
mutation"
198. .203
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/label= x2
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Pred. No. 1e-87;
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lkins JA;
                                                             region,
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diagnosis; t
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                                                                with Cys81Ser
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Best Local S
Matches 171
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07-NOV-1996.
07-NOV-1996.
22-APR-1996; U05611.
02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-431644.
07-JUN-1995; US-482114.
07-JUN-1995; US-4
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01-FEB-1997
MP4 chimera
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A 21.5 kDa foetal isoform (W06108) of myelin basic protein, MBP+X2Ser81/bact., is the product of a DNA construct (T41897) based on the human foetal MBP+X2Cys81 isoform (W00399) but utilising codons that are highly expressed in bacterial genes 1 place of the native codons (see also T41889) and incorporating sequence coding for a hexa-histidine tail. This allows large-scale prodn. and purification of the MBP in bacterial hosts. Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) useful in the clinical assessment, diagnosis and treatment of MSP Sequence 203 AA;
                                                                                                                                                                                                                                                                                                                                                                                MP4 chimera (MBP21.5-delta PLP4 fusion).

Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP; MBP21.5; multiple sclerosis; autoimmune disease; diagnosis; therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.
                                                                      domain
                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                       protein
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/Label= Spacer
201. .373
/label= Delta_PLP4
201. .205
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/note= "the hexa-histidine tag facilitates
purification of the recombinant protein
from host cells"
                                                                                                                                         /label- MBP21.
198. .200
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Pred. No. 1e-87;
0; Mismatches 0
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W09634622-A1.
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22-APR-1996; U05611.
02-MAY-1995; US-431644.
02-MAY-1995; US-431644.
07-JUN 1995; US-431641.
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/label- E
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the native protein"
208. .219
                                                          /label= Histidine_tag
/note= "hexa-histidine
protein purification"
                                                                                                                                         /label= Epitope
/note= "encephalitogenic
256, 269
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/note= "PLP epitope
326. .339
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/note= "PLP epitope
295. .306
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/note= "PLP epitope
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/note= "PLP epitope
257. .269
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/note= "PLP epitope
256. .269
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/note= "PLP epitope
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/note= "PLP epitope
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Claim 34; Page 110-112; 156pp; English.

CMP4 chimera (W06103) is a fusion protein composed of human myelin CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and CC delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lacks CC all 4 hydrophobic domains of native human PLP (W06106) but CC includes PLP epitopes associated with multiple sclerosis (MS). It CC can be expressed in E. coli transformants using a DNA construct CC (T41893) contg. the MBP21.5 delta PLP4 gene fusion. MP4 chimera CC and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08) CC are useful for the clinical assessment, diagnosis and treatment
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Best Local S
Matches 171
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22-MAY-1995; US-431644.

02-MAY-1995; US-431644.

07-JUN-1995; US-482114.

(ALEX-) ALEXION PHARM INC.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McFarland HF, Mueller EF
Nye SH, Pelirey CM, Squinto SP, Wilkins JA;
WPI; 96-50898/50.
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Synthetic.
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Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
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Proteolipid protein; PLP; delta PLP4; myelin basi
MBP21.5; multiple sclerosis; autoimmune disease;
therapy; T-lymphocyte; T-cell; MMOGP4 chimera;
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Claim 33; Page 108-110;
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O; Mismatches
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.3e-87
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                scierosis
Claim 36; Page 115-117; 156pp; English.
MMOGP4 chimera (W06105) is a fusion protein composed of human myelin basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the extracellular domain of human myelin oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutein.
MBP21.5, PLP and MOG are all recognised by autoreactive T cells from multiple scierosis (MS) patients. The chimera was produced using a DNA construct (T41895) obtd. by inserting a sequence encoding the MOG molety into MP4 chimera DNA (see also T41893). MMOGP4 chimera
                                                                                                                                                                                                       (ALEX-)
(USSH)
Lenardo
Nye SH,
WPI; 96-
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                                                                                                                                                           New human myelin basic used in the assessment,
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07-JUN-1995;
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02-MAY-1995;
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/note= "hexa-histidine
protein purification"
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/note= "encephalitogenic
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/note= "PIP epitope associated with
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Proteolipid
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mes 171; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                           era (delta PLP4-MBP21.5 fusion).
pid protein; PLP; delta PLP4; myelin basic protein;
multiple sclerosis; autoimmune disease; diagnosis;
T-lymphocyte; T-cell; PM4 chimera.
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                       58. .71
/label= Epitope
/late= "PLP epitope a
/label Epitope
/note "PLP epit
71. .104
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/note "PLP epitope
57. 70
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49. .70
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42. .62
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11. .3
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/note= "PLP epitope
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/note= "PLP epitope
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                                                                                                                              /label=
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the native protein"
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                                                     Query Match
Best Local Sin
Matches 170;
                                                 Claim 35; Page 113-114; 156pp; English.

PM4 chimera (W06104) is a fusion protein composed of delta PLP4 (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein (PLP) mutein that lacks all 4 hydrophobic domains of native human PLP (W06106) but includes PLP epitopes associated with multiple sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic protein (MBP) associated with MS. PM4 is in reverse orientation to MP4 chimera (W06103). It can be expressed in bacterial host cells using a DNA construct (T41894). PLP polypeptides (see also W00400, W06101-03 and W06105) can be used in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ, Matis L, McFarland HF, Mueller
Nye SH, Pelirey CM, Squinto SP, Wilkins JA;
WPI; 96-505898/50.
                                                                                                                                                                                                                                               22-APR-1996; U05611.
02-MAY-1995; US-431648.
02-MAY-1995; US-431644.
07-JUN-1995; US-482114.
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       Similarity 86.
70; Conservative
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protein purification"
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/note= "PLP epitope
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/note= "PLP epitope
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Pred. No. 7.4e-87;
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RESULT
R04717
ID R0.
AC R0.
DT 23:
DE Emg
KW Mye
KW ep:
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Best Local (
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23-APR-1992; U03391.
23-APR-1991; US-690840.
(AMER-) AMERGEN INC.
(Clark BR, Lerch BL, Sh
WPI; 93-036056/04.
                 R04717 standard; protein; 168 A
R04717:
23-AUG-1990 (first entry)
Empirically determined sequence
Myelin basic protein; multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immune response such as auto immunity
Claim 30; Page 68 + Fig 7; 93pp; English.
A method is claimed for the prepn. of a pure major MHC-peptide complex. The MHC component is a Class II glycoprotein of the and the peptide comprises amino acids 1-14 of MBP.

Sequence 170 AA;
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epitope; myelin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pure major MHC-peptide complex - useful in treating
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107
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                         sequence of myelin basic protein (MBP) multiple sclerosis; autoantigen; automm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "claim 30;
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.9e-87;
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pT antigen specific T helper cells
pS Fig 7; 74pp; English.

CC The patent claims complexes of formulae (1), (II) and (III) which are as
pS Fig 7; 74pp; English.

CC follows: (I) X - MCH - peptide; (II) MHC - peptide - X; (III) MHC -
pC follows: (I) X - MCH - peptide; (II) MHC - peptide includes an
pPT instruction of the major autoimmune diseases, including
pPT instruction of the major autoinmune diseases, including
pPT instruction in the complexes which can be used to
pRT candidate peptide for insertion in the complexes which can be used to
pPT instruction of mice which develops experimental
pPT in p94717 is with the substitution of the residues above the
pRT and an in p94717 is with the substitution of the residues above the
pRT and an in p92226.

CC camence in Fig 7. The sequence without substitutions is given in p92226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 164; Conserv
                                                                                                                                               03-MAR-1994.
17-AUG-1993; U07786.
17-AUG-1992; US-931217.
(AUTO-) AUTOIMMUNE INC.
Hafler DA, Welher HL;
WPI; 94-082786/10.
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28-DEC-1989.
23-JUN-1989;
21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                  Rabbit myelin basic protein.

Proteolipid protein; myelin basic protein; retrovirus; proteolipid protein; myelin basic protein; TGF-beta; neurological disease; by-standar antigen; TGF-beta; transforming growth factor-beta; T-cell; T-lymphocyte; myelopathy; paraparesis; human immunodeficiency virus oryctolagus cuniculus.
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misc_difference
                           Treating retroviral associated neurological of by stander antigen, causing release of tractor beta from suppressor T cells pisclosure; Page 49; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R48594 standard; protein;
R48594;
31-JUL-1994 (first entry)
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proteins (sequences R48592-96)
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/note-"Arg-COOH"
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Pred. No. 3.7e-83;
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                                                                                  al disease - )
transforming
and cattle proteolipid
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Search completed: September 26, 2000, 19:25:03
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